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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 04:57:07 ; Search time 534 Seconds
(without alignments)
9275.219 Million cell updates/sec

Title: US-10-024-444B-1

Sequence: 1 gcaactaaaacacatca.....ttccacgctctagggaagga 977

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3340653 seqs, 2534783454 residues

Word size : 20

Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

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19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	977	100.0	977	15	US-10-024-444B-1
2	720	73.7	1033	15	US-10-017-161-635
3	120	12.3	951	9	US-09-886-055-198
4	120	12.3	951	10	US-09-804-291-198
5	120	12.3	951	13	US-10-343-650A-513
6	120	12.3	951	15	US-10-220-382-39
7	120	12.3	951	16	US-10-300-846-25
8	120	12.3	1008	10	US-09-974-591-11
9	120	12.3	1008	10	US-09-974-591-13
10	120	12.3	1008	10	US-09-974-789-10
11	120	12.3	1008	10	US-09-974-149-11
12	120	12.3	1008	10	US-09-974-149-13
13	120	12.3	1050	10	US-09-777-789-8
14	120	12.3	1351	15	US-10-017-161-309

ALIGNMENTS

15	120	12.3	1351	16	US-10-292-798-275	Sequence 275, App
16	88	9.0	507	10	US-09-777-789-45	Sequence 45, App1
17	88	9.0	528	10	US-09-777-789-40	Sequence 40, App1
18	27	2.8	678	15	US-10-259-430-45	Sequence 45, App1
19	27	2.8	678	15	US-10-259-423-45	Sequence 45, App1
20	27	2.8	912	16	US-10-300-846-15	Sequence 15, App1
21	26	2.7	26	15	US-10-024-444B-11	Sequence 11, App1
22	26	2.7	26	16	US-10-024-212-251	Sequence 251, App1
23	26	2.7	932	10	US-09-907-218-17	Sequence 835, App1
24	26	2.7	1337	15	US-10-017-161-835	Sequence 843, App
25	26	2.7	1337	15	US-10-017-161-843	Sequence 717, App
26	26	2.7	1337	16	US-10-292-798-717	Sequence 113, App
27	25	2.6	950	15	US-10-023-597-113	Sequence 101286,
28	25	2.6	1113	13	US-10-027-632-101286	Sequence 101286,
29	25	2.6	1113	16	US-10-027-632-101286	Sequence 987, App
30	25	2.6	1250	15	US-10-017-161-987	Sequence 843, App
31	25	2.6	1250	16	US-10-292-798-843	Sequence 1301, App
32	23	2.4	931	15	US-10-017-161-1301	Sequence 1069, App
33	23	2.4	931	16	US-10-292-798-1069	Sequence 3, App1
34	23	2.4	939	15	US-10-027-417-3	Sequence 95, App1
35	23	2.4	939	16	US-10-023-597-95	Sequence 95, App1
36	23	2.4	945	15	US-10-023-597-95	Sequence 134, App
37	23	2.4	945	16	US-10-300-846-13	Sequence 134, App
38	23	2.4	951	9	US-09-886-055-134	Sequence 283, App
39	23	2.4	951	10	US-09-804-291-134	Sequence 21, App1
40	23	2.4	951	13	US-10-343-650A-283	Sequence 115, App1
41	23	2.4	951	16	US-10-387-629-21	Sequence 23, App1
42	23	2.4	962	15	US-10-023-597-23	Sequence 21, App1
43	23	2.4	963	15	US-10-023-597-23	Sequence 49, App1
44	23	2.4	971	13	US-10-433-581-21	
45	23	2.4	980	15	US-10-023-806-49	

RESULT 1
US-10-024-444B-1
Sequence 1, Application US/10024444B
Publication No. US20030165858A1

GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Gerlach, Valerie L.
APPLICANT: Smithson, Glenda
APPLICANT: Stone, David
APPLICANT: Bin-Yang, Ruey
APPLICANT: Conley, Pamela B.
APPLICANT: Hart, Matthew
APPLICANT: Tomlinson, James E.
APPLICANT: Topper, James N.
APPLICANT: Kekuda, Ramesh
APPLICANT: Caeman, Stacie J.
APPLICANT: Macdougall, John R.
APPLICANT: Shlomit, Edinger R.
TITLE OF INVENTION: Same
FILE REFERENCE: 21402-224 AG
CURRENT APPLICATION NUMBER: US//10/024,444B
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/256635
PRIOR FILING DATE: 2000-12-18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 977
TYPE: DNA
ORGANISM: Human
US-10-024-444B-1

Query Match 100.0%; Score 977; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GCAACTAAAAACACATCATGAGAGCTCCGGAACTCCACCTTGGGAGAGGCTTCATCT 60
Db 1 GCAACTAAAAACACATCATGAGAGCTCCGGAACTCCACCTTGGGAGAGGCTTCATCT 60
Qy 61 GGTGGGGATTCGATGAGAGAGGCTCTCTGAACTGCTCTATGCTACATTTACATCT 120
Db 61 GGTGGGGATTCGATGAGAGAGGCTCTCTGAACTGCTCTATGCTACATTTACATCT 120
Qy 121 ATACATGTTGGAGTACGACGAGCAATGCTGCTGCTCCGAGCATACCATGAAAGCCGG 180
Db 121 ATACATGTTGGAGTACGACGAGCAATGCTGCTGCTCCGAGCATACCATGAAAGCCGG 180
Qy 181 GCTCCACATGCCCATGATGATCTCTGCTGGGAGCTCTCTCATGAGACCTCTGTTAC 240
Db 181 GCTCCACATGCCCATGATGATCTCTGCTGGGAGCTCTCTCATGAGACCTCTGTTAC 240
Qy 241 ATCTGTTGCTACCTCCCAAGGCTTGGGAGCTTCTGGGCAAGAAACATATCTCTT 300
Db 241 ATCTGTTGCTACCTCCCAAGGCTTGGGAGCTTCTGGGCAAGAAACATATCTCTT 300
Qy 301 TGGAGGCTGTGCACTTCAAGATGTTCTGGCACTGACAAATGGGTAGGAGGAGCTCT 360
Db 301 TGGAGGCTGTGCACTTCAAGATGTTCTGGCACTGACAAATGGGTAGGAGGAGCTCT 360
Qy 361 ACTGACCTTCATGAGCTTATGACAGGATGATGAGCAATTTGTCACTCTGAAATACATGAC 420
Db 361 ACTGACCTTCATGAGCTTATGACAGGATGATGAGCAATTTGTCACTCTGAAATACATGAC 420
Qy 421 CCTATGAGCCCAAGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 CCTATGAGCCCAAGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy 481 GATTGCTATGAGCACTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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Qy 541 CAGGATCTGCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 CAGGATCTGCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 601 GATGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 GATGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 661 TGTGGCTCTCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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Qy 721 GAAAGAAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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Qy 781 TGCCACATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
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Qy 841 CTCTGTTTCTACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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Qy 901 TAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 TAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 961 CAGGCTTAGGAGAGGA 977
Db 961 CAGGCTTAGGAGAGGA 977

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RESULT 2
 US-10-017-161-635
 ; Sequence 635, Application us/10017161
 ; Publication No. US2003014368A1

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; GENERAL INFORMATION:
; APPLICANT: SUMI, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKITAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 08435/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
; LENGTH: 1033
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1033)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(833)
US-10-017-161-635

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Query Match 73.7%; Score 720; DB 15; Length 1033;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 1 ACCAGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
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Qy 197 TACCTCTGCTTGGGAGCTCTCTCTATGAGACTCTCTCTGTTCACTCTGTTGCTACCTCC 256
Db 61 TACCTCTGCTTGGGAGCTCTCTCTATGAGACTCTCTCTGTTCACTCTGTTGCTACCTCC 120
Qy 257 AAGGCTTGGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
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Db 121 AAGGCTTGGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 179
Qy 317 CAGATGTTCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376
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Db 180 CAGATGTTCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 239
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Db 240 TATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
Qy 437 GTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 496
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Db 300 GTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
Qy 497 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 556
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Db 360 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
Qy 557 GAGATGCCACCTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
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Db 420 GAGATGCCACCTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
Qy 617 TACGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 676
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Db 480 TACGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
Qy 677 CTAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736
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Db 540 CTAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599
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Db 600 ACCGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 659

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Qy	857	ATTGTCAC	TC	CCAGCCCTG	AATCCATCT	CTACAGCCTG	AGAAATAAGAGGTC	ATGCGG	916
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Qy	917	GCCTTGAG	AGAGGGCTCTCTG	GGAAATAATCAT	ACTGCTGG	CACATTC	CACAGCTCT	TAGGAAAG	976
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Qy	977	A	977						
Db	840	A	840						

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RESULT 3
US-09-886-055-198
; Sequence 198. Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886, 055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-886-055-198

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Query Match	12.3%	Score 120	DB 9	Length 951
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Matches	120	Conservative	0	Mismatches 0; Indels 0; Gaps 0

QY	826	ACAAAGACAACATCATCTCTGTTTTCTACACAAATGTCTCACTCCAGCCCTGAATCCACTCAT	885
Db	807	ACAAAGACAACATCATCTCTGTTTTCTACACAAATGTCTCACTCCAGCCCTGAATCCACTCAT	866
QY	886	CTACAGCCTGAGGAATTAAGAGGTCATGCGGGCCTTTGAGAGGGTCTCTGGGAAAAATACAT	945
Db	867	CTACAGCCTGAGGAATTAAGAGGTCATGCGGGCCTTTGAGAGGGTCTCTGGGAAAAATACAT	926

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RESULT 4
US-09-804-291-198
; Sequence 198, Application US/09804291
; Publication No. US2003008805A1
; GENERAL INFORMATION:
; APPLICANT: ZOZOLA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/139,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849

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; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-291-198

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[illegible]

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RESULT 5
US-10-343-650A-513
; Sequence 513. Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343, 650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
;
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(951)
US-10-343-650A-513

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Query Match Similarity      12.3%; Score 120; DB 13; Length 951;
Best Local Similarity      100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      826  ACAGACAACATCATCTCTGTTTTCACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Qy      886  CTACAGCCTGAGGAATTAAAGAGGTATGCGGGCCTTTGAGGAGGGTCTCGGAAATAATCAT 945
Db      867  CTACAGCCTGAGGAATTAAAGAGGTATGCGGGCCTTTGAGGAGGGTCTCGGAAATAATCAT 926

RESULT 6
US-10-220-382-39
; Sequence 39, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: IAL, Pirelli

```

APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandra
APPLICANT: YAO, Monique G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: LU, Dying, Aina M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junning
APPLICANT: HARLAND, Lee
APPLICANT: WALSH, Rodrick T.
APPLICANT: LO, Terence P.
APPLICANT: BOROMSKY, Mark L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0044 PCT
CURRENT FILING DATE: 2001-03-01
CURRENT FILING DATE: 2001-03-01
PRIOR FILING DATE: 60/186,854; 60/188,384; 60/190,453; 60/190,730
PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 39
LENGTH: 951
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030119111A1 7472446CBI
US-10-220-382-39

Query Match 12.3%; Score 120; DB 15; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
DB 807 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATCGGCGCTTGAGAGGGTCTCTGGGAAATATCAT 945
DB 867 CTACAGCCTGAGGAATTAAGAGGTCATCGGCGCTTGAGAGGGTCTCTGGGAAATATCAT 926

RESULT 7
US-10-300-846-25
Sequence 25, Application US/10300846
Publication No. US2003020737A1
GENERAL INFORMATION:
APPLICANT: HAN, YI
APPLICANT: ZOUZYLA, SERGEY
APPLICANT: ECHSEVERI, FERNANDO
APPLICANT: WANG, KUN
TITLE OF INVENTION: OLFACTORY RECEPTORS FOR ISOVALENIC ACID AND RELATED
TITLE OF INVENTION: MALODORANTS AND USE THEREOF IN ASSAYS FOR
FILE REFERENCE: 078003-0291924
CURRENT FILING DATE: 2002-11-21
CURRENT FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 951
TYPE: DNA
ORGANISM: Homo sapiens
US-10-300-846-25

Query Match 12.3%; Score 120; DB 16; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
DB 807 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATCGGCGCTTGAGAGGGTCTCTGGGAAATATCAT 945
DB 867 CTACAGCCTGAGGAATTAAGAGGTCATCGGCGCTTGAGAGGGTCTCTGGGAAATATCAT 926

RESULT 8
US-09-974-591-11
Sequence 11, Application US/09974591
Publication No. US20030059830A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Burgess, Catherine E
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly A
TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfactory
TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
TITLE OF INVENTION: the Same
FILE REFERENCE: 15966-654 CIP
CURRENT FILING DATE: 2001-10-09
CURRENT FILING DATE: 2001-10-09
PRIOR FILING DATE: 60/245,292
PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 1008
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (27) .. (998)
US-09-974-591-11

Query Match 12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
DB 857 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATCGGCGCTTGAGAGGGTCTCTGGGAAATATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGGTCATCGGCGCTTGAGAGGGTCTCTGGGAAATATCAT 976

RESULT 9
US-09-974-591-13
Sequence 13, Application US/09974591
Publication No. US20030059830A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Burgess, Catherine E
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly A
TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfactory
TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
TITLE OF INVENTION: the Same
FILE REFERENCE: 15966-654 CIP
CURRENT FILING DATE: 2001-10-09
CURRENT FILING DATE: 2001-10-09
PRIOR FILING DATE: 60/245,292
PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1008
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (27) .. (998)
US-09-974-591-13

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; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(998)
US-09-974-591-13

Query Match          12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
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DB 857 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

QY 886 CTACAGCCTGAGGAATTAAGAGAGTCAATGCGGCGCTTGAGAGAGGTCTCGGAAATATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGAGTCAATGCGGCGCTTGAGAGAGGTCTCGGAAATATCAT 976

RESULT 10
US-09-777-789-10
; Sequence 10, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-654
; CURRENT APPLICATION NUMBER: US/09/777,789
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/180,646
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-789-10

Query Match          12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
DB 857 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

QY 886 CTACAGCCTGAGGAATTAAGAGAGTCAATGCGGCGCTTGAGAGAGGTCTCGGAAATATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGAGTCAATGCGGCGCTTGAGAGAGGTCTCGGAAATATCAT 976

RESULT 11
US-09-974-149-11
; Sequence 11, Application US/09974149
; Publication No. US20030175705A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Bader, Joel S
; APPLICANT: Bansal, Aruna
```

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; TITLE OF INVENTION: Methods of Use for No. US20030175705A1el Single Nucleotide
; TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
; TITLE OF INVENTION: and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-654UB
; CURRENT APPLICATION NUMBER: US/09/974,149
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/323,755
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(998)
US-09-974-149-11

Query Match          12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 886 CTACAGCCTGAGGAATTAAGAGAGTCAATGCGGCGCTTGAGAGAGGTCTCGGAAATATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGAGTCAATGCGGCGCTTGAGAGAGGTCTCGGAAATATCAT 976

RESULT 12
US-09-974-149-13
; Sequence 13, Application US/09974149
; Publication No. US20030175705A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Bader, Joel S
; APPLICANT: Bansal, Aruna
; TITLE OF INVENTION: Methods of Use for No. US20030175705A1el Single Nucleotide
; TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
; FILE REFERENCE: 15966-654UB
; CURRENT APPLICATION NUMBER: US/09/974,149
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/323,755
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(998)
US-09-974-149-13

Query Match          12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db 917 CTACAGCTGAGGAATTAAGAGGTCTATGCGGCTTGAGAGGGTCTCTGGAAAAATTCAT 976

RESULT 13
US-09-777-789-8
; Sequence 8, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:

; APPLICANT: Padigar et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-654
; CURRENT APPLICATION NUMBER: US/09/777,789
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/180,646
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-789-8

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Best Local Similarity 100.0%; Pred. No. 2.1e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

US-10-017-161-309
; Sequence 309, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: AURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 309
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; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: source
; LOCATION: (1) .. (1351)
; FEATURE:
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US-10-017-161-309

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Best Local Similarity 100.0%; Pred. No. 2.1e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACACATCATCTCTGTTTCTACACAAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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QY 886 CTACAGCTGAGGAATTAAGAGGTCTATGCGGCTTGAGAGGGTCTCTGGAAAAATTCAT 945
DB 1067 CTACAGCTGAGGAATTAAGAGGTCTATGCGGCTTGAGAGGGTCTCTGGAAAAATTCAT 1126

RESULT 15
US-10-292-798-275
; Sequence 275, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:

; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: AURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 275
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
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; LOCATION: (1) .. (1351)
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US-10-292-798-275

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Best Local Similarity 100.0%; Pred. No. 2.1e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACACATCATCTCTGTTTCTACACAAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Search completed: October 6, 2004, 06:53:02
Job time : 536 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 5, 2004, 14:24:16 ; Search time 130 Seconds
(without alignments)
782.220 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1 MELRNSTLGGFVLVGLIND.....VWRALRYLVGYLLAHSTL 316

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	316	100.0	316	US-10-024-444B-2	Sequence 2, Appl1
2	210	66.5	210	US-10-017-161-636	Sequence 636, App
3	57	18.0	316	US-09-886-055-197	Sequence 197, App
4	57	18.0	316	US-09-777-789-9	Sequence 9, Appl1
5	57	18.0	316	US-09-804-291-197	Sequence 197, App
6	57	18.0	316	US-09-912-976-53	Sequence 53, Appl1
7	57	18.0	316	US-09-965-422-58	Sequence 58, Appl1
8	57	18.0	316	US-10-343-650A-514	Sequence 514, App
9	57	18.0	316	US-10-220-382-18	Sequence 18, Appl1
10	57	18.0	316	US-10-017-161-310	Sequence 310, App
11	57	18.0	316	US-10-024-444B-3	Sequence 3, Appl1
12	57	18.0	316	US-10-300-846-26	Sequence 26, Appl1
13	57	18.0	324	US-10-292-798-276	Sequence 276, App
14	57	18.0	324	US-09-974-591-12	Sequence 12, Appl1
15	57	18.0	324	US-09-974-591-14	Sequence 14, Appl1

16	57	18.0	324	US-09-777-789-11	Sequence 11, Appl1
17	57	18.0	324	US-09-974-149-12	Sequence 12, Appl1
18	57	18.0	324	US-09-974-149-14	Sequence 14, Appl1
19	43	13.6	316	US-09-912-976-50	Sequence 50, Appl1
20	43	13.6	316	US-09-912-976-51	Sequence 51, Appl1
21	43	13.6	316	US-09-965-422-60	Sequence 60, Appl1
22	43	13.6	316	US-10-024-444B-5	Sequence 5, Appl1
23	43	13.6	316	US-10-024-444B-6	Sequence 6, Appl1
24	29	9.2	316	US-09-795-271-51	Sequence 51, Appl1
25	29	9.2	316	US-10-024-444B-4	Sequence 4, Appl1
26	28	8.9	316	US-09-777-789-41	Sequence 41, Appl1
27	28	8.9	316	US-09-777-789-42	Sequence 42, Appl1
28	28	8.9	316	US-09-777-789-46	Sequence 46, Appl1
29	28	8.9	316	US-09-777-789-47	Sequence 47, Appl1
30	28	8.9	316	US-09-795-271-48	Sequence 48, Appl1
31	28	8.9	316	US-09-912-976-52	Sequence 52, Appl1
32	28	8.9	316	US-09-965-422-56	Sequence 56, Appl1
33	28	8.9	316	US-10-024-444B-7	Sequence 7, Appl1
34	28	8.9	316	US-10-005-041A-104	Sequence 104, App
35	23	7.3	319	US-09-795-271-50	Sequence 50, Appl1
36	23	7.3	319	US-09-965-422-57	Sequence 57, Appl1
37	17	5.4	315	US-09-795-271-49	Sequence 49, Appl1
38	17	5.4	315	US-09-965-422-59	Sequence 59, Appl1
39	17	5.4	315	US-09-981-566A-71	Sequence 71, Appl1
40	17	5.4	315	US-10-005-041A-105	Sequence 105, App
41	15	4.7	316	US-10-023-597-68	Sequence 68, Appl1
42	14	4.4	317	US-09-886-055-201	Sequence 201, App
43	14	4.4	317	US-09-804-291-201	Sequence 201, App
44	14	4.4	317	US-09-907-218-2	Sequence 2, Appl1
45	14	4.4	317	US-09-907-218-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-10-024-444B-2
; Sequence 2, Application US/10024444B
; Publication No. US20030165858A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Smithson, Glennda
; APPLICANT: Stone, David
; APPLICANT: Bin-Yang, Ruey
; APPLICANT: Conley, Pamela B.
; APPLICANT: Hart, Matthew
; APPLICANT: Tomlinson, James E.
; APPLICANT: Topper, James N.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Casman, Stacey J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Shlomit, Edinger R.
; TITLE OF INVENTION: No. US20030165858A1el GPCR-Like Proteins and Nucleic Acids Encod
; FILE REFERENCE: 21402-224 AG
; CURRENT APPLICATION NUMBER: US/10/024,444B
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/256635
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Human
US-10-024-444B-2
Query Match 100.0%; Score 316; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.6e-284; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0

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Db      301 LRRVIGKYILLAHSTL 316

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RESULT 2

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US-10-017-161-636
; Sequence 636, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABORATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 064335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 636
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-636

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Query Match      66.5%; Score 210; DB 14; Length 210;
Best Local Similarity 100.0%; Pred. No. 3.3e-186;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-886-055-197
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; Patent No. US20020132273A1
; GENERAL INFORMATION:

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; APPLICANT: STRYER, LOBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-197

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RESULT 4

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US-09-777-789-9
; Sequence 9, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-654
; CURRENT APPLICATION NUMBER: US/09/777,789
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/180,646
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-789-9

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Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-804-291-197
; Sequence 197, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24

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; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-197

Query Match      18.0%; Score 57; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      52 EARLHMPYLLLGQSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108
Db      52 EARLHMPYLLLGQSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108

RESULT 6
US-09-912-976-53
; Sequence 53, Application US/09912976
; Publication No. US20030212255A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mezes, Peter
; APPLICANT: Burgess, Catherine
; APPLICANT: Caeman, Stracie
; APPLICANT: Grosse, William M
; APPLICANT: Alshbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Mishra, Vishnu
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-070
; CURRENT APPLICATION NUMBER: US/09/912,976
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/221,336
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/238,333
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/260,675
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/271,025
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/278,164
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/280,876
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-976-53

Query Match      18.0%; Score 57; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      52 EARLHMPYLLLGQSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108
Db      52 EARLHMPYLLLGQSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108
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Db      52 EARLHMPYLLLGQSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108

RESULT 7
US-09-965-422-58
; Sequence 58, Application US/09965422
; Publication No. US20030216545A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Caeman, Stracie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine
; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Taylor, Sarah
; APPLICANT: Gunther, Erik
; APPLICANT: Tchertev, Vellizar T
; TITLE OF INVENTION: No. US20030216545A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-422-58

Query Match      18.0%; Score 57; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      52 EARLHMPYLLLGQSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108
Db      52 EARLHMPYLLLGQSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108

RESULT 8
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US-10-343-650A-514
; Sequence 514, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 514
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-514

Query Match 18.0%; Score 57; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPWTLIGQLSLMDLFTSVTPKALADFLRENTISFGGALOMFLATWG 108
DB 52 EARLHMPWTLIGQLSLMDLFTSVTPKALADFLRENTISFGGALOMFLATWG 108

* RESULT 9

US-10-220-382-18
; Sequence 18, Application US/10220382
; Publication No. US2003011911A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULET, Catherine
; APPLICANT: LU, Dying Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROMSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/10/220,382
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US2003011911A1 7472446CD1
US-10-220-382-18

Query Match 18.0%; Score 57; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPWTLIGQLSLMDLFTSVTPKALADFLRENTISFGGALOMFLATWG 108
DB 52 EARLHMPWTLIGQLSLMDLFTSVTPKALADFLRENTISFGGALOMFLATWG 108

RESULT 10
US-10-017-161-310
; Sequence 310, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 08435/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 310
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-310

Query Match 18.0%; Score 57; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPWTLIGQLSLMDLFTSVTPKALADFLRENTISFGGALOMFLATWG 108
DB 52 EARLHMPWTLIGQLSLMDLFTSVTPKALADFLRENTISFGGALOMFLATWG 108

RESULT 11
US-10-024-444B-3
; Sequence 3, Application US/1002444B
; Publication No. US20030165858A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Smithson, Glenda
; APPLICANT: Stone, David
; APPLICANT: Bin-Yang, Ruey
; APPLICANT: Conley, Pamela B.
; APPLICANT: Hart, Matthew
; APPLICANT: Tomlinson, James E.
; APPLICANT: Topper, James N.
; APPLICANT: kekuda, Ramesh
; APPLICANT: Casman, Stacie J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Shlomit, Edinger R.
; TITLE OF INVENTION: No. US20030165858A1 GPCR-Like Proteins and Nucleic Acids Encodir
; FILE REFERENCE: 21402-224 AG
; CURRENT APPLICATION NUMBER: US/10/024,444B
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/256635
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 316
; TYPE: PRT
; ORGANISM: human
US-10-024-444B-3

Query Match 18.0%; Score 57; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108
DB 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108

RESULT 12

US-10-300-846-26
; Sequence 26, Application US/10300846
; Publication No. US2003020737A1
; GENERAL INFORMATION:
; APPLICANT: HAN, YI
; APPLICANT: ZOUJIYA, SERGEY
; APPLICANT: ECHEVERRI, FERNANDO
; APPLICANT: WANG, KUN
; TITLE OF INVENTION: OLFACTORY RECEPTORS FOR ISOVALERIC ACID AND RELATED
; TITLE OF INVENTION: MALODORANTS AND USE THEREOF IN ASSAYS FOR
; TITLE OF INVENTION: IDENTIFICATION OF BLOCKERS OF MALODOR
; FILE REFERENCE: 078003-0291924
; CURRENT APPLICATION NUMBER: US/10/300,846
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/348,371
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 09/809,291
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/341,872
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-846-26

Query Match 18.0%; Score 57; DB 15; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108
DB 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108

RESULT 13

US-10-292-798-276
; Sequence 276, Application US/10292798
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 276
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-276

Query Match 18.0%; Score 57; DB 15; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108
DB 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108

RESULT 14

US-09-974-591-12
; Sequence 12, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfacto
; TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
; TITLE OF INVENTION: the Same
; FILE REFERENCE: 15966-654 CIP
; CURRENT APPLICATION NUMBER: US/09/974,591
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-591-12

Query Match 18.0%; Score 57; DB 10; Length 324;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108
DB 60 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 116

RESULT 15

US-09-974-591-14
; Sequence 14, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfacto
; TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
; TITLE OF INVENTION: the Same
; FILE REFERENCE: 15966-654 CIP
; CURRENT APPLICATION NUMBER: US/09/974,591
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-591-14

Query Match 18.0%; Score 57; DB 10; Length 324;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPYLLIGQLSMDLFTSVTPKALADFLRRENTISFGGALQMFALTMG 108

Wed Oct 6 10:49:29 2004

us-10-024-444b-2.011.rapb

Page 6

Db 60 BARLHMPVLLIGQLSLMDLIFTSVTPKALADFLRRENTISFGGALQMFALTMG 116

Search completed: October 5, 2004, 14:36:23
Job time : 131 secs

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 03:17:06 ; Search time 2511 Seconds
(without alignments)
11619.016 Million cell updates/sec

Title: US-10-024-444B-1
Perfect score: 977
Sequence: 1 gcaactataaaacacatca.....ttccacgcctagggaagga 977

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues
Word size : 20

Total number of hits satisfying chosen parameters: 94

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
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2: em_estbm:*
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18: em_gss_inv:*
19: em_gss_pla:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	121	12.4	710	AG031161 Pan trogl
2	89	9.1	29	AG090554 Pan trogl
3	84	8.6	28	AG0522745 HS_5221_B
4	43	4.4	10	BE897401 BE897401 601437394

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
AG031161	LOCUS	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	DEFINITION	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	ACCESSION	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	VERSION	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	KEYWORDS	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	SOURCE	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	ORGANISM	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	REFERENCE	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	TITLE	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	JOURNAL	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								
AG031161	COMMENT	Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.	AG031161								

ALIGNMENTS

710 bp DNA linear GSS 01-NOV-2001
Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.
AG031161
AG031161.1 GI:16558034
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
2 (bases 1 to 710)
Unpublished
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:Chimpbes@gsr.riken.go.jp, URL:http://jngp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of

ORIGIN

ECORI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcorI sites"

Query Match 8.6%; Score 84; DB 28; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAAGGGGCTTCACTCTGTTGGGATTCGATGACAGTGGTCTCCTGAACCTGCTTATG 104
DB 432 GAAGGGGCTTCACTCTGTTGGGATTCGATGACAGTGGTCTCCTGAACCTGCTTATG 491
QY 105 CTACATTACATTCCTATACATGT 128
DB 492 CTACATTACATTCCTATACATGT 515

RESULT 4
BE897401 843 bp mRNA linear EST 20-OCT-2000
LOCUS 601437394F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922342 5',
DEFINITION mRNA sequence.
ACCESSION BE897401
VERSION BE897401.1 GI:10362826
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: LHAM9756 row: 1 column: 23
High quality sequence start: 12
High quality sequence stop: 614.
Location/Qualifiers

FEATURES
Source
1. 843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3922342"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI, Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 4.4%; Score 43; DB 10; Length 843;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 TTTCCTCTGCTCCCATTTCTGTCATTTGGCTCTCTACACA 676
DB 129 TTTCCTCTGCTCCCATTTCTGTCATTTGGCTCTCTACACA 171

RESULT 5
AZ373068 625 bp DNA linear GSS 02-OCT-2000
LOCUS AZ373068.1
DEFINITION 1M0125N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION clone UUGC1M0125N08 F, genomic survey sequence.
VERSION AZ373068
KEYWORDS AZ373068.1 GI:10486768
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
MUS musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 625)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std. Error: 0.00
Plate: 0125 Row: N Column: 08
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 625.
Location/Qualifiers

FEATURES
Source
1. 625
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0125N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.9%; Score 38; DB 28; Length 625;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 ATGGCCTATGACAGGTATGTGGCCATTTGTCTATCTCT 408
DB 255 ATGGCCTATGACAGGTATGTGGCCATTTGTCTATCTCT 218

RESULT 6
AZ806221 455 bp DNA linear GSS 20-FEB-2001
LOCUS AZ806221.1
DEFINITION 2M0068B10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION	musculus cDNA clone 2032D01 5', mRNA sequence.
VERSION	CB174035
KEYWORDS	CB174035.1 GI:37592664
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Bases 1 to 528)
TITLE	Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Friddy, L., Ross, J.A., Walker, M., Williams, E.M. and Traak, B.J. Olfactant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels
JOURNAL	Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT	Contact: Young JM Traak Lab, Division of Human Biology Fred Hutchinson Cancer Research Center 1100 Fairview Avenue N., C3-166, P.O. Box 19024, Seattle, WA 98109-1024, USA Tel: 206 667 1471 Fax: 206 667 6524 Email: jayyoung@fhcrc.org Young gene new name GA_x6K027Q025-47640742-47639798 Young gene old name GA_x5U8B7MKXV-147900-146844 Zhang gene name MOR185-4 Seq primer: M13 Reverse.

FEATURES	Location/Qualifiers
source	1. .528

Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org

Young gene new name GA x6K02T20125-47640742-47639798
Young gene old name GA x5J8B7M3KV-147900-148844
Zhang gene name MOR185-4
Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

```
1..595
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2028D09"
/cisue_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
/note="Organ: Olfactory turbinates; Vector:
lambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Leslie Vossahl. mRNA was prepared from
the Olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector."
```

ORIGIN

Query Match 3.2%; Score 31; DB 14; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 CATGGCCTATGACAGTATGGCCATTGT 400
|||||
Db 386 CATGGCCTATGACAGTATGGCCATTGT 416

RESULT 9

AZ323827/c

LOCUS 432 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0045B03R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0045B03 R, genomic survey sequence.

ACCESSION AZ323827
VERSION AZ323827.1 GI:10378931
KEYWORDS GSS.

SOURCE

Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinger, A., von
Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: B column: 03

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 432.

FEATURES
SOURCE
1..432
Location/Qualifiers
/organism="Mus musculus"

```
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0045B03"
/sex="Male"
```

```
//lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: pMD229v; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gt10/4732114[3d]/AF12072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
```

ORIGIN

Query Match 2.9%; Score 28; DB 28; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TCATGGCCTATGACAGTATGTGCCAT 396
|||||
Db 250 TCATGGCCTATGACAGTATGTGCCAT 223

RESULT 10

BH352344

LOCUS 545 bp DNA linear GSS 03-DEC-2001
DEFINITION CH230-136E3 TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-136E3, genomic survey sequence.

ACCESSION BH352344
VERSION BH352344.1 GI:17283078
KEYWORDS GSS.

SOURCE

Rattus norvegicus (Norway rat)

REFERENCE

AUTHORS

1 (bases 1 to 545)
Zhao, S., Shetty, J., Shatman, S., Teegaye, G., Geer, K.,
Shvartsbeyn, A., Geeregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rac230.htm). For BAC library
availability, please contact Pieter de Jong (pje@chomgmai1.chomg.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
plate: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Seq primer: T7
Class: BAC ends.

FEATURES
SOURCE
1..432
Location/Qualifiers
/organism="Mus musculus"

source

1. .545
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SnHsd/MCw"
/db_xref="taxon:10116"
/clone="CH230-136E3"
/sex="Female"
/cell_type="Brain"
/clone_1ib="CHORI-230 Segment 1"
/note="Vector: PTARBAC2.1; Site 1: ECORI; Site 2: ECORI; CHORI-230 Rat (BN/SnHsd/MCw) BAC library produced by Pieter de Jong"

ORIGIN

Query Match 2.9%; Score 28; DB 28; Length 545;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TCATGGCCTATGACAGTATGTGCCCAT 396
|||||
212 TCATGGCCTATGACAGTATGTGCCCAT 239

RESULT 11
LOCUS A2709687 680 bp DNA linear GSS 24-JAN-2001
DEFINITION RPCI-24-82P2.TV RPCI-24 Mus musculus genomic clone RPCI-24-82P2,
ACCESSION A2709687
KEYWORDS genomic survey sequence.
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 680)
Zhao,S., Nieman,W., Malek,J., Shateman,S., Akturet,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorsis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-82P2.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1. .680
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-82P2"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_1ib="RPCI-24"
/note="Vector: PTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the PTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male CS7BL/6J
DNA."

ORIGIN

ORIGIN

Query Match 2.9%; Score 28; DB 28; Length 680;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 CATGGCCTATGACAGTATGTGCCATT 397
|||||
463 CATGGCCTATGACAGTATGTGCCATT 436

Db

RESULT 12
LOCUS BF444685 222 bp mRNA linear EST 01-DEC-2000
DEFINITION 262681 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF444685
VERSION BF444685.1 GI:11504777
KEYWORDS EST.
SOURCE Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 222)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Perrea,G., Sultana,R.,
Quackenbush,J. and Keeler,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
MEDLINE 12226715
PUBMED

JOURNAL
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
Email: smith@meat.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 98 row: G column: 8
Seq primer: ATTAGGACACATATAG.
Location/Qualifiers
1. .222
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1ib="MARC 2P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES
source

ORIGIN

Query Match 2.7%; Score 26; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 881 CTCATCTACAGCCTGAGGAATTAAGA 906
|||||
Db 157 CTCATCTACAGCCTGAGGAATTAAGA 182

RESULT 13
LOCUS AM486191 334 bp mRNA linear EST 09-JUL-2000
DEFINITION 71360 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AM486191
VERSION AM486191.1 GI:7056297
KEYWORDS EST.

SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 334)
 AUTHORS Fahrentkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Quackenbush, J., and Keele, J.W.
 TITLE Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
 JOURNAL Mamm. Genome 13 (8), 475-478 (2002)
 MEDLINE 22213789
 PUBMED 12226715
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 20 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
 Plate: 30 row: D column: 6
 Seq primer: ATTAGTGACACTATG.
 Location/Qualifiers
 1..334
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 1Pig"
 /note="Vector: PCWV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

ORIGIN
 Query Match 2.7%; Score 26; DB 10; Length 334;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 881 CTCATCTACAGCCTGAGATAAGGA 906
 |||||
 90 CTCATCTACAGCCTGAGATAAGGA 115

RESULT 14
 BZ949576 387 bp DNA linear GSS 13-JUN-2003
 LOCUS CH240.3809.TV CHORI-240 Bos taurus genomic clone CH240_3809,
 DEFINITION genomic survey sequence.
 ACCESSION BZ949576
 VERSION BZ949576.1 GI:31734881
 KEYWORDS GSS.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 387)
 AUTHORS Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A.
 TITLE A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence
 JOURNAL Unpublished (2003)
 COMMENT Contact: Harris Lewin
 Department of Animal Sciences
 University of Illinois at Urbana Champaign
 1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.choi.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by the University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative)
 Plate: 38 row: 0 column: 9
 Seq primer: 17
 Class: BAC ends.
 Location/Qualifiers
 1..387
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="bred: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_3809"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull 11 Domingo 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN
 Query Match 2.7%; Score 26; DB 28; Length 387;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 884 ATCTACAGCCTGAGATAAGGAGT 909
 |||||
 222 ATCTACAGCCTGAGATAAGGAGT 247

RESULT 15
 B1399100/c 451 bp mRNA linear EST 14-AUG-2001
 LOCUS MI-P-AV1-nrk-c-11-0-UI-s1 MI-P-AV1 Sus scrofa cDNA clone
 DEFINITION MI-P-AV1-nrk-c-11-0-UI 3', mRNA sequence.
 ACCESSION B1399100
 VERSION B1399100.1 GI:15178161
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 451)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Tuglie CK
 Molecular Genetics Laboratory, Department of Animal Science
 Iowa State University
 201 Kiddie Hall, Ames, IA 50011-3150, USA
 Tel: 5152944252
 Fax: 5152942401
 Email: ctuglie@iastate.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized placenta library cDNA library preparation. M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University

of Iowa Clone distribution: clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=yes.

FEATURES

source

Location/Qualifiers
 1. 451

/organism="Sus scrofa"
 /mol_type="rRNA"
 /strain="crossbreed"
 /db_xref="taxon:9823"
 /clone="MI-P-Ayl-nrk-c-11-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="MI-P-Ayl"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ayl
 library is normalized library derived from the MI-P-Ayl
 library, ultimately derived from placenta tissue. For a
 detailed description of the library from which this clone
 was derived, please visit our web site at
<http://piglet.genome.iastate.edu/>. The procedure used to
 create this library has been previously described
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
 1996)
 TAG TISSUE=placenta
 TAG LIB=MI-P-Ayl
 TAG_SEQ=ATTGG"

ORIGIN

Query Match

Best Local Similarity 2.7%; Score 26; DB 12; Length 451;
 Pred. No. 0.054;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 881 CTCATCTACAGCCTGAGGATAAGA 906

DB 61 CTCATCTACAGCCTGAGGATAAGA 36

Search completed: October 6, 2004, 05:39:08
 Job time : 2521 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 01:54:16 ; Search time 3864 Seconds

(without alignments)
10959.147 Million cell updates/sec

Title: US-10-024-444B-1

Perfect score: 977

Sequence: 1 gcaactaaaaaacacatca.....ttccacgctcagggaagga 977

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 20

Total number of hits satisfying chosen parameters: 679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

GenEmbl:*

1: gb_da:*

2: gb_hhg:*

3: gb_in:*

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15: em_da:*

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17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hhg_hum:*

31: em_hhg_inv:*

32: em_hhg_other:*

33: em_hhg_mus:*

34: em_hhg_pln:*

35: em_hhg_rod:*

36: em_hhg_mam:*

37: em_hhg_vrt:*

38: em_sy:*

39: em_hhg_hum:*

40: em_hhg_mus:*

41: em_hhg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	977	100.0	977	6	AX686711	AX686711 Sequence	
C 2	89.6	211735	9	AC091564	AC091564 Homo sapi	C	
3	856	87.6	1350	9	AB065539		AB065539 Homo sapi
C 4	856	87.6	208430	2	AC027641		AC027641 Homo sapi
5	827	84.6	947	6	AX241682		AX241682 Sequence
6	605	61.9	649	9	AF399487		AF399487 Homo sapi
7	120	12.3	948	6	AX241679		AX241679 Sequence
8	120	12.3	951	6	AX244613		AX244613 Sequence
9	120	12.3	951	6	AX448455		AX448455 Sequence
10	120	12.3	951	6	BD144532		BD144532 Novel G-P
11	120	12.3	1008	6	AX210250		AX210250 Sequence
12	120	12.3	1008	6	AX551018	AX551018 Sequence	
13	120	12.3	1008	6	AX551020	AX551020 Sequence	
14	120	12.3	1050	6	AX210248	AX210248 Sequence	
15	120	12.3	1351	6	AX646083	AX646083 Sequence	
C 16	120	12.3	1351	9	AB065823	AB065823 Homo sapi	C
17	120	12.3	171660	2	AC017103	AC017103 Homo sapi	
18	120	12.3	173611	9	AC087280	AC087280 Homo sapi	
19	120	12.3	211735	9	AC091564	AC091564 Homo sapi	
20	88	9.0	507	6	AX210285	AX210285 Sequence	
21	88	9.0	528	6	AX210280	AX210280 Sequence	
C 22	88	9.0	111126	9	AF321237	AF321237 Homo sapi	
23	64	6.6	650	9	AF399618	AF399618 Homo sapi	
24	50	5.1	948	10	AY073646	AY073646 Mus muscu	
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27	50	5.1	239821	2	AC098982	AC098982 Rattus no	
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36	41	4.2	951	10	AY073056	AY073056 Mus muscu	
37	41	4.2	951	10	AY317826	AY317826 Mus muscu	
38	41	4.2	954	10	AY073498	AY073498 Mus muscu	
39	41	4.2	954	10	AY317818	AY317818 Mus muscu	
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ALIGNMENTS

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LOCUS	AX686711				
DEFINITION	Sequence 1 from Patent WO02070707.				
ACCESSION	AX686711				
VERSION	AX686711.1	GI:29372291			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Padigar,M., Gerlach,V.L., Smithson,G., Stone,D., Bin-Yang,R., Conley P., Hart,M., Tomlinson,J.E., Topper,J.N., Kekuda,R., Casman,S.J., Edinger,S. and MacDougall,J.R.				

Pred. No. is the number of results predicted by chance to have a

TITLE Gpcr-like proteins and nucleic acids encoding same
JOURNAL Patent: WO 02070707-A 1 12-SEP-2002;
Curagen Corporation (US); COR THERAPEUTICS, INC. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 977; DB 6; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCACCTAAAAAACACATCATGAGAGCTCCGGAACCTCTTGGAAGCGCTTCATCTT 60

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DB 61 GGTGGGGATTCTGATGACAGTGGGTCCTGAACTGCTATGCTATTAACATCTT 120

QY 121 ATACATGTTGGACACTGACAGCAATGCTGCTGCTGCTGAGCCATCACCATAGAACCCG 180
DB 121 ATACATGTTGGACACTGACAGCAATGCTGCTGCTGCTGAGCCATCACCATAGAACCCG 180

QY 181 GCTCCACATGCCCATGTAACCTCCCTGCTGGGAGAGTCTCTCATGAGCCCTGTTTAC 240
DB 181 GCTCCACATGCCCATGTAACCTCCCTGCTGGGAGAGTCTCTCATGAGCCCTGTTTAC 240

QY 241 ATCTGTTGTCACCTCCCAAGGCTTGGGGAATTTCTGCGCAGAGAAAAACATATCTCTT 300
DB 241 ATCTGTTGTCACCTCCCAAGGCTTGGGGAATTTCTGCGCAGAGAAAAACATATCTCTT 300

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QY 361 ACTGGCCCTTACAGGCTTGAAGAGTATGAGTGGCAATTTGATCTCTGAAATACATGAC 420
DB 361 ACTGGCCCTTACAGGCTTGAAGAGTATGAGTGGCAATTTGATCTCTGAAATACATGAC 420

QY 421 CCTCATGAGCCCAAGAGTCTGCTGATCATGATGAGTGGCAATCTTGATCTGATCTCT 480
DB 421 CCTCATGAGCCCAAGAGTCTGCTGATCATGATGAGTGGCAATCTTGATCTGATCTCT 480

QY 481 GATTGCTATAGGACATACCATGATACATATGACACTCTCTTCTGCTGCTGAGAAAT 540
DB 481 GATTGCTATAGGACATACCATGATACATATGACACTCTCTTCTGCTGCTGAGAAAT 540

QY 541 CAGGCATCTGCTCTGTGATGCCACCTGCTGTAAGTGGCTGCTGATACCTCTCAG 600
DB 541 CAGGCATCTGCTCTGTGATGCCACCTGCTGTAAGTGGCTGCTGATACCTCTCAG 600

QY 601 GTATGAGCTTAAATATATACGTAGACAGTGTGACTTCTCTTCTGCTCCCATTTCTGCAT 660
DB 601 GTATGAGCTTAAATATATACGTAGACAGTGTGACTTCTCTTCTGCTCCCATTTCTGCAT 660

QY 661 TGTGGCCCTCCACACACATAGTCTTATCTGCTGCTGATGCTCATTAATGAGGGAG 720
DB 661 TGTGGCCCTCCACACACATAGTCTTATCTGCTGCTGATGCTCATTAATGAGGGAG 720

QY 721 GAAGAAGACCTTGTACCTGCTCTTCCACATGATGTTGGTGGGAGTGTCTATGAGGC 780
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QY 901 TAAGAGGTCTATGCGGCGCTTGAGAGAGGTCCTGGGAAAAATACATCTGTCGACATTC 960
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QY 961 CAGCCTCTAGGGAAGA 977
DB 961 CAGCCTCTAGGGAAGA 977

RESULT 2

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LOCUS Homo sapiens chromosome 11, clone RP11-732A19, complete sequence.
DEFINITION AC091564
AC091564.12 GI:22657585
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Birren,B., Nussbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 11, clone RP11-732A19
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 211735)

Birren,B., Linton,L., Nussbaum,C., Lander,E., Allen,N., Anderson,S.,
Barra,N., Bastien,V., Boguslavsky,L., Bouknight,B., Brown,A.,
Camarata,J., Campiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collamore,A., Cooke,P., DeRellano,K., Dewar,K.,
Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardina,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Hatford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., Larocque,K.,
Lamazares,R., Landers,T., Lenoczky,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheters,R., Meldrum,J., Meneus,L.,
Mhova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rhee,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Schojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S.,
Theodore,J., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

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320

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3

(bases

1 to

211735)

Barron,B.,

Nussbaum,C.,

Lander,E.,

Ali,A.,

Allen,N.,

Anderson,S.,

Barra,N.,

Bastien,V.,

Boguslavsky,L.,

Bouknight,B.,

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Dodge,S.,

Fero,S.,

Ferreira,P.,

Fitzgerald,M.,

Gage,D.,

Galagan,J.,

Gardina,S.,

Ginde,S.,

Goyette,M.,

Graham,L.,

Grand-Pierre,N.,

Hagos,B.,

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Horton,L.,

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Landers,T.,

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Seaman,S.,

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Viel,R.,

Vo,A.,

Wilson,B.,

Wu,X.,

Wyman,D.,

Young,G.,

Zainoun,J.,

Zembek,L.,

Zimmer,A.

and

Zody,M.

Direct

Submission

Submitted

(07-MAY-2001)

Whitehead

Institute/MIT

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(bases

1 to

211735)

TITLE

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REFERENCE

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4

(bases

1 to

211735)

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, L., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karakas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, U., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zahoun, J., Zemdek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL

Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 3, 2002 this sequence version replaced g1:22123080.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

COMMENT

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: 111860
Center clone name: 732_A_19

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      721     GAAGAAAGCCCTGTGCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
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QY      781     TGGCAATTCATGATGATGTTGCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
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Db      165514 CAGGCTCTAGGGAAGA 165498

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RESULT 3
AB065539      1350 bp      DNA      linear      PRI 23-JUL-2002
LOCUS        Homo sapiens gene for seven transmembrane helix receptor,
DEFINITION   isolate:CBRC7TM_102.
ACCESSION    AB065539

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VERSION      AB065539.1 GI:21928374
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
              Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.
              Genome-wide discovery and analysis of human seven transmembrane
              helix receptor genes
              Unpublished
              2 (bases 1 to 1350)
              Suwa,M.
JOURNAL      Direct Submission
AUTHORS      Submitted (11-JUN-2001) Makiko Suwa, Computational Biology Research
              Center (CBRC), National Institute of Advanced Industrial Science
              and Technology (AIST), 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
              (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
              Tel:81-3-3599-8080, Fax:81-3-3599-8081)
COMMENT      This sequence is a seven transmembrane helix receptor candidate
              predicted from the whole human genome sequences using our automated
              system that contains programs of gene
              finding(GeneDecoder), sequence search, motif-domain assignment and
              transmembrane helix prediction.
              And the sequence is submitted by the collaborative project between
              Computational Biology Research Center (CBRC), National Institute
              of Advanced Industrial Science and Technology (AIST) and [Genome
              Science Division, Research Center for Advanced Science and
              Technology (RCAST), University of Tokyo].
FEATURES     Location/Qualifiers
             source          1..1350
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                           /chromosome="11"
             misc_feature    201..1150
                           /product="seven transmembrane helix receptor"
                           /evidence="not_experimental"
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Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;
Matches 976; Conservative
QY      1      GCAACTAATAAACAATCATGAGAGCTCCGAACTCCACTTGGGAAGCGGCTTCAATCTT 60
Db      182     GCAACTAATAAACAATCATGAGAGCTCCGAACTCCACTTGGGAAGCGGCTTCAATCTT 241
QY      61      GGTGGGAGATTCATGATGACAGTGGGTCTCTGAACTGCTCTATGCTATTAACATCTT 120
Db      242     GGTGGGAGATTCATGATGACAGTGGGTCTCTGAACTGCTCTATGCTATTAACATCTT 301
QY      121     ATACATGTTGGACACTGACACAGCAATGCTGCTGCTCTGCGCAATCAACATAGAAGCCG 180
Db      302     ATACATGTTGGACACTGACACAGCAATGCTGCTGCTCTGCGCAATCAACATAGAAGCCG 361
QY      181     GCTCCACATGCCCATGATGATCTCTGCTGCTGCGAGCTCTCTCATGAGACCTCTGTTAC 240
Db      362     GCTCCACATGCCCATGATGATCTCTGCTGCTGCGAGCTCTCTCATGAGACCTCTGTTAC 421
QY      241     ATCTGTTGTCATCTCCCAAGGCTTGGCGACTTCTTGGCGAGAAAACATATCTCTCT 300
Db      422     ATCTGTTGTCATCTCCCAAGGCTTGGCGACTTCTTGGCGAGAAAACATATCTCTCT 480
QY      301     TGGAGGCTGTGCACTTCAATGTTCTCTGCGCACTGACCAATGGGTAGGGCTGAGGACCTCT 360
Db      481     TGGAGGCTGTGCACTTCAATGTTCTCTGCGCACTGACCAATGGGTAGGGCTGAGGACCTCT 540
QY      361     ACTGGCCTTCATGAGCTTATGACAGGTATGTCGCAATTTGTCATCTCTGAAAATACATGAC 420
Db      541     ACTGGCCTTCATGAGCTTATGACAGGTATGTCGCAATTTGTCATCTCTGAAAATACATGAC 600

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Query Match      87.6%; Score 856; DB 2; Length 208430;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 976; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 GCACCTAAAAAACAATCATGAGCTCCGGAACCTCCAGTGGAGGCGCTTCATCTT 60
DB      52629 GCACCTAAAAAACAATCATGAGCTCCGGAACCTCCAGTGGAGGCGCTTCATCTT 52570
QY      61 GGTGGGATTTCTGATGATGACAGTGGGCTCTCTGAATGCTCTATGCTAATTAAATCCT 120
DB      52569 GGTGGGATTTCTGATGATGACAGTGGGCTCTCTGAATGCTCTATGCTAATTAAATCCT 52510
QY      121 ATACATGTTGGACTGACCAAGCATATGCTGCTGCTCTGCGCATACCACTAGAGCCG 180
DB      52509 ATACATGTTGGACTGACCAAGCATATGCTGCTGCTCTGCGCATACCACTAGAGCCG 52450
QY      181 GCTCCACATGCCCATGATACCTCGCTTGGGAGCTCTCTCATGAGACCTCTGTTAC 240
DB      52449 GCTCCACATGCCCATGATACCTCGCTTGGGAGCTCTCTCATGAGACCTCTGTTAC 52390
QY      241 ATCTGTTGCTACTCCCAAGGCTTGGCGAATTCTTGGCGAGAGAAAACATATCTCTT 300
DB      52389 ATCTGTTGCTACTCCCAAGGCTTGGCGAATTCTTGGCGAGAGAAAACATATCTCTT 52331
QY      301 TGAAGGCTGTCACCTTCAATGTTCTCTGGACATGACATGAGGCTGAGGACCTCCT 360
DB      52330 TGAAGGCTGTCACCTTCAATGTTCTCTGGACATGAGGCTGAGGACCTCCT 52271
QY      361 ACTGAGCCTTATGAGCTGATGACAGTATGTTGGCATTGTCATCTCTGAAATACATGAC 420
DB      52270 ACTGAGCCTTATGAGCTGATGACAGTATGTTGGCATTGTCATCTCTGAAATACATGAC 52211
QY      421 CCTCATGAGCCCAAGAGCTGCTGATGATGATGAGGCAATCTCTGATCTGCGATCTCCT 480
DB      52210 CCTCATGAGCCCAAGAGCTGCTGATGATGATGAGGCAATCTCTGATCTGCGATCTCCT 52151
QY      481 GATTGCTATAGAGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB      52150 GATTGCTATAGAGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 52091
QY      541 CAGGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

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DB      52090 CAGGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 52031
QY      601 GTATGAGCTTATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 660
DB      52030 GTATGAGCTTATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 51971
QY      661 TGTGGCCCTCTACACACTAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB      51970 TGTGGCCCTCTACACACTAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 51911
QY      721 GAAGAAAGCCCTTGTACCTGCTCTTCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB      51910 GAAGAAAGCCCTTGTACCTGCTCTTCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 51851
QY      781 TGCCACATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB      51850 TGCCACATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 51791
QY      841 CTCTGTTTCTACACAAATTTGCTACCTCAGCCTGATTCATCTACATCTACATCTACATCTACATCTACATCT 900
DB      51790 CTCTGTTTCTACACAAATTTGCTACCTCAGCCTGATTCATCTACATCTACATCTACATCTACATCT 51731
QY      901 TTAGAGGCTATGCGGCGCTTGAAGAGGCTCTGCGGAAATACATGATGATGATGATGATGATGATGATGATGAT 960
DB      51730 TTAGAGGCTATGCGGCGCTTGAAGAGGCTCTGCGGAAATACATGATGATGATGATGATGATGATGATGAT 51671
QY      961 CACGCTCTAGGAGAGGA 977
DB      51670 CACGCTCTAGGAGAGGA 51654

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RESULT 5
AX241682      947 bp      DNA      linear      PAT 26-SEP-2001
LOCUS      AX241682
DEFINITION      Sequence 430 from Patent WO0127158.
ACCESSION      AX241682
VERSION      AX241682.1 GI:15798557
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Bellensohn, J., Smith, D., Lancet, D., Glusman, G., Fuchs, T. and Yanai, I.
TITLE
JOURNAL
PATENT
DIGISCENTS
FEATURES
source
1.947
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ORIGIN

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Query Match      84.6%; Score 827; DB 6; Length 947;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 947; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      20 ATGAGGCTCCGGAACCTGACCTTGGAGGCGCTTCACTTGGGAGATTCGATGAC 79
DB      1 ATGAGGCTCCGGAACCTGACCTTGGAGGCGCTTCACTTGGGAGATTCGATGAC 60
QY      80 AGTGGGCTCTCTGAACTGCTATGCTAATTTCATATATATATATATATATATATATATATATATATATATATAT 139
DB      61 AGTGGGCTCTCTGAACTGCTATGCTAATTTCATATATATATATATATATATATATATATATATATATATATAT 120
QY      140 AGCAATGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199
DB      121 AGCAATGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY      200 CTCCTGCTTGGGAGAGCTCTCTCATGAGACCTCTGTTCAATCTGTTGTCATCTCCAAAG 259

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TITLE	Lehrach, H., Olander, Z., Glusman, G., Lancet, D. and Shamir, R.			
JOURNAL	Submitted (16-JUL-2001) Dept. of Molecular Genetics and the Crown Human Genome Center, Weizmann Institute of Science, Rehovot 76100, Israel			
FEATURES	Location/Qualifiers			
source	1..649			
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="OR2A2P" 1..5649 /gene="olfactory receptor" /note="contains transmembrane regions 2-7" /pseudo			
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Best Local Similarity	100.0%;	Pred 0.0;	Mismatches 0;	Indels 0;
Matches 605;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	266	GCGGACTTTTGGCGAGAGAAAACTATCTCTTGGAGGCTGTGACCTTCAGATGTTCT	325	
Db	45	GCGGACTTTTCTGGCGAGAGAAAACTATCTCTTCTTGGAGGCTGTGACCTTCAGATGTTCT	104	
QY	326	CTGGCACTACATAGGGGTAGGGCTAGAGCCCTCCATCGGCTTTATGAGCTTATGACAGG	385	
Db	105	CTGGCACTACATAGGGGTAGGGCTAGAGCCCTCCATCGGCTTTATGAGCTTATGACAGG	164	
QY	386	TATGTGGCCATTGTTCATCTCTGAATAATACGACCCCTATGAGCCCAAGAGTCGTGG	445	
Db	165	TATGTGGCCATTGTTCATCTCTGAATAATACGACCCCTATGAGCCCAAGAGTCGTGG	224	
QY	446	ATCATGTGGGCCACATCTCTGATCTCTGCAATCTCTGATTTGCTATAGACATATCCATGTAC	505	
Db	225	ATCATGTGGGCCACATCTCTGATCTCTGCAATCTCTGATTTGCTATAGACATATCCATGTAC	284	
QY	506	ACTATGCACTCCCTTTCTGTGTGTCCTGGGAATACAGGCATCTGCTGTGAGATCCCA	565	
Db	285	ACTATGCACTCCCTTTCTGTGTGTCCTGGGAATACAGGCATCTGCTGTGAGATCCCA	344	
QY	566	CCCTTGTCTGAAGTTGGCTGTGCTGATACCTTCAGATGAGCTTATATATTAAGTGACA	625	
Db	345	CCCTTGTCTGAAGTTGGCTGTGCTGATACCTTCAGATGAGCTTATATATTAAGTGACA	404	
QY	626	GGTGTGACCTTCCTCTGTCCTGCCATTTCTGSCCATTTGTGGCTCTTACACATAGTCTTA	685	
Db	405	GGTGTGACCTTCCTCTGTCCTGCCATTTCTGSCCATTTGTGGCTCTTACACATAGTCTTA	464	
QY	686	TTCACTGTGCTTGTATGAGCCATCAATATGAGGGGAGAAAGAGCCCTGTACCTGCTCT	745	
Db	465	TTCACTGTGCTTGTATGAGCCATCAATATGAGGGGAGAAAGAGCCCTGTACCTGCTCT	524	
QY	746	TCCCACTCGATTGTGTGTGGGATGTTCTTATGAGAGCTGCCACATTCATGTAATGCTTGCC	805	
Db	525	TCCCACTCGATTGTGTGTGGGATGTTCTTATGAGAGCTGCCACATTCATGTAATGCTTGCC	584	
QY	806	AGTTCCTTCCACAGCCCCCAACAAGACAATATCTCTGTTTCTACACATTTGTCACT	865	
Db	585	AGTTCCTTCCACAGCCCCCAACAAGACAATATCTCTGTTTCTACACATTTGTCACT	644	
QY	866	CCAGC 870		
Db	645	CCAGC 649		
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LOCUS	AX241679	948 bp	DNA	linear
DEFINITION	Sequence 427 from Patent WO0127158.			
ACCESSION	AX241679			
VERSION	AX241679.1	GI:15798554		
KEYWORDS				

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bellenson, J., Smith, D., Lancel, D., Glusman, G., Fuchs, T. and Yanai, I.
TITLE Olfactory receptor sequences
JOURNAL Patent: WO 0127158-A 427 19-APR-2001;
Doligents (US); YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
FEATURES
SOURCE location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="(H389276 nucleotide)"

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Query Match 12.3%; Score 120; DB 6; Length 948;
Best Local Similarity 100.0%; Pred. No. 2.8e-58; Indels 0; Gaps 0;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCATCCAGCCCTGAATCCACTCAT 885
DB 807 ACAAGACAATCATCTCTGTTTCTACACAATTGTCATCCAGCCCTGAATCCACTCAT 866
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAAGAGGTCCTGGGAAATATACAT 945
DB 867 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAAGAGGTCCTGGGAAATATACAT 926

RESULT 8
AX244613 951 bp DNA linear PAT 28-SEP-2001
LOCUS AX244613
DEFINITION Sequence 39 from Patent WO0166742.
ACCESSION AX244613
VERSION AX244613.1 GI:15859514
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Lal, P., Tang, Y. T., Patterson, C., Yao, M. G., Shih, L. L., Tribouley, C. M., Lu, D. A., Yue, H., Khan, F. A., Policky, J. L., Au-Yang, J., Yang, J., Harland, L., Walsh, R. T., Lo, T. P. and Borowsky, M. L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0166742-A 39 13-SEP-2001;
Incyte Genomics, Inc. (US)
FEATURES
SOURCE location/Qualifiers
1..951
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/note="Incyte ID No: 7472446CB1"

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Query Match 12.3%; Score 120; DB 6; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.8e-58; Indels 0; Gaps 0;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCATCCAGCCCTGAATCCACTCAT 885
DB 807 ACAAGACAATCATCTCTGTTTCTACACAATTGTCATCCAGCCCTGAATCCACTCAT 866
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAAGAGGTCCTGGGAAATATACAT 945
DB 867 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAAGAGGTCCTGGGAAATATACAT 926

RESULT 9
AX448455 951 bp DNA linear PAT 03-JUL-2002
LOCUS AX448455

DEFINITION Sequence 121 from Patent WO0224726.
AX448455
ACCESSION AX448455.1 GI:21697353
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velthuis, A.
TITLE Olfactory and pheromones G-protein coupled receptors
JOURNAL Patent: WO 0224726-A 121 28-MAR-2002;
ChemCom S.A. (BE)
FEATURES
SOURCE location/Qualifiers
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/db_xref="taxon:9606"
1..951
/note="unnamed protein product"
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/db_xref="GI:21697354"
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VYTHMYPGCAQRIHRLCEI,PHILKVAQATSRLELVYMGVTFLLPSLAITIAS
TOILITVLMPSNEGRKALVTCSSHLVVMFGAATFMYLVPSFSHTODNITIS
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ORIGIN
Query Match 12.3%; Score 120; DB 6; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.8e-58; Indels 0; Gaps 0;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAATTGTCATCCAGCCCTGAATCCACTCAT 885
DB 807 ACAAGACAATCATCTCTGTTTCTACACAATTGTCATCCAGCCCTGAATCCACTCAT 866
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAAGAGGTCCTGGGAAATATACAT 945
DB 867 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAAGAGGTCCTGGGAAATATACAT 926

RESULT 10
BD144532 951 bp DNA linear PAT 17-JAN-2003
LOCUS BD144532
DEFINITION Novel G-protein coupled receptors.
ACCESSION BD144532
VERSION BD144532.1 GI:27850290
KEYWORDS Novel G-protein coupled receptors
SOURCE JP 2002112793-A/257.
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Haga, T., Takeda, S. and Miyake, N.
TITLE Novel G-protein coupled receptors
JOURNAL Patent: JP 2002112793-A 257 16-APR-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002112793-A/257
PD 16-APR-2002
PF 09-FEB-2001 JP 2001034434
PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE
PC C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K39/395, A61K45/00, PC
A61K48/00,
PC A61P43/00, C07K14/705, C07K16/28, C07K19/00, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
G01N33/566//

FEATURES
source
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC Novel G-protein coupled receptors
FH Key Location/Qualifiers
CDS (1)..(951).
1..951
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 12.3%; Score 120; DB 6; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACATCATCTCTGTTTCTACACAAATGTCACGCCCTGAATCCACTCAT 885
DB 807 ACAAGACATCATCTCTGTTTCTACACAAATGTCACGCCCTGAATCCACTCAT 866
QY 886 CTACAGCCTGAGGAATTAAGAGGTGATGCGGCGCTTGAGGAGAGGTCTCTGGAAATAATCAT 945
DB 867 CTACAGCCTGAGGAATTAAGAGGTGATGCGGCGCTTGAGGAGAGGTCTCTGGAAATAATCAT 926

RESULT 11

AX210250 1008 bp DNA linear PAT 31-AUG-2001
LOCUS AX210250
DEFINITION Sequence 10 from Patent WO0157215.
ACCESSION AX210250
VERSION AX210250.1 GI:15424571
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
1 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Padigaru, M., Spytek, K.A., Li, L., Ballinger, R.A., Mishra, V.S. and Baumgartner, J.C.
TITLE Novel polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0157215-A 10 09-AUG-2001;
FEATURES
source
Location/Qualifiers
1..1008
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 12.3%; Score 120; DB 6; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACATCATCTCTGTTTCTACACAAATGTCACGCCCTGAATCCACTCAT 885
DB 857 ACAAGACATCATCTCTGTTTCTACACAAATGTCACGCCCTGAATCCACTCAT 916
QY 886 CTACAGCCTGAGGAATTAAGAGGTGATGCGGCGCTTGAGGAGAGGTCTCTGGAAATAATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGGTGATGCGGCGCTTGAGGAGAGGTCTCTGGAAATAATCAT 976

RESULT 12

AX551018 1008 bp DNA linear PAT 26-NOV-2002
LOCUS AX551018
DEFINITION Sequence 11 from Patent WO0236632.
ACCESSION AX551018
VERSION AX551018.1 GI:25814023
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS
Alsbrook, J.P., Burgess, C.E., Grosse, W.M., Lepley, D.M., Padigaru, M. and Spytek, K.A.
TITLE Novel single nucleotide polymorphisms for olfactory receptor-like polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0236632-A 11 10-MAY-2002;
CDS Curagen Corporation (US)
FEATURES
source
Location/Qualifiers
1..1008
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
27..1001
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD57894.1"
/db_xref="GI:25814024"
/db_xref="REMBL:CAD57894"
/translation="MELMNYHSMELMNTLGSGLTIVGLINDSGSPILLICATITLIL
LALISNGLLAIITWEARLHMPVLLIGLSIMDLFTSVTPPKALDPLRENTISF
GGCALQWFLALTMGAEDLLAFNAYIDRYVAICHPITWTLMSSRAWLMATWILA
SLSLIIVYVTHMHPFCAOEIRHLICIPHLKACADTSRYELMVMVGVTFILPS
LAALIASYQILLTVLHMPNMEGRKKALVTCSSHLTVGMFYGAATFMYVLPSSPHST
RQDNISVYFIVTIPALNPLIYSIRNKEVMALRVLGKWLPAHSTL"

ORIGIN

Query Match 12.3%; Score 120; DB 6; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACATCATCTCTGTTTCTACACAAATGTCACGCCCTGAATCCACTCAT 885
DB 857 ACAAGACATCATCTCTGTTTCTACACAAATGTCACGCCCTGAATCCACTCAT 916
QY 886 CTACAGCCTGAGGAATTAAGAGGTGATGCGGCGCTTGAGGAGAGGTCTCTGGAAATAATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGGTGATGCGGCGCTTGAGGAGAGGTCTCTGGAAATAATCAT 976

RESULT 13

AX551020 1008 bp DNA linear PAT 26-NOV-2002
LOCUS AX551020
DEFINITION Sequence 13 from Patent WO0236632.
ACCESSION AX551020
VERSION AX551020.1 GI:25814025
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
1 Alsbrook, J.P., Burgess, C.E., Grosse, W.M., Lepley, D.M., Padigaru, M. and Spytek, K.A.
TITLE Novel single nucleotide polymorphisms for olfactory receptor-like polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0236632-A 13 10-MAY-2002;
CDS Curagen Corporation (US)
FEATURES
source
Location/Qualifiers
1..1008
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
27..1001
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD57895.1"
/db_xref="GI:25814026"
/db_xref="REMBL:CAD57895"
/translation="MELMNYHSMELMNTLGSGLTIVGLINDSGSPILLICATITLIL
LALISNGLLAIITWEARLHMPVLLIGLSIMDLFTSVTPPKALDPLRENTISF
GGCALQWFLALTMGAEDLLAFNAYIDRYVAICHPITWTLMSSRAWLMATWILA
SLSLIIVYVTHMHPFCAOEIRHLICIPHLKACADTSRYELMVMVGVTFILPS
LAALIASYQILLTVLHMPNMEGRKKALVTCSSHLTVGMFYGAATFMYVLPSSPHST
RQDNISVYFIVTIPALNPLIYSIRNKEVMALRVLGKWLPAHSTL"

ORIGIN

Query Match 12.3%; Score 120; DB 6; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAAATGTCACTCCAGCCCTGAATCCACTCAT 885
DB 857 ACAAGACAATCATCTCTGTTTCTACACAAATGTCACTCCAGCCCTGAATCCACTCAT 916
QY 886 CTACAGCCTGAGGAATAGAGGTCAATGCGGCGCTTGAGAGAGGCTCTGGGAAAATACAT 945
DB 917 CTACAGCCTGAGGAATAGAGGTCAATGCGGCGCTTGAGAGAGGCTCTGGGAAAATACAT 976

RESULT 14

LOCUS AX210248 1050 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 8 from Patent WO0157215.
ACCESSION AX210248
VERSION AX210248.1 GI:15424570
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Padigaru, M., Spytek, K.A., Li, L., Ballinger, R.A., Mishra, V.S. and
Baumgartner, J.C.

TITLE Novel polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0157215-A 8 09-AUG-2001;
Curagen Corporation (US)

FEATURES Location/Qualifiers
source 1..1050
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 12.3%; Score 120; DB 6; Length 1050;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAAATGTCACTCCAGCCCTGAATCCACTCAT 885
DB 878 ACAAGACAATCATCTCTGTTTCTACACAAATGTCACTCCAGCCCTGAATCCACTCAT 937
QY 886 CTACAGCCTGAGGAATAGAGGTCAATGCGGCGCTTGAGAGAGGCTCTGGGAAAATACAT 945
DB 938 CTACAGCCTGAGGAATAGAGGTCAATGCGGCGCTTGAGAGAGGCTCTGGGAAAATACAT 997

RESULT 15

LOCUS AX646083 1351 bp DNA linear PAT 04-MAR-2003
DEFINITION Sequence 275 from Patent EP1270724.
ACCESSION AX646083
VERSION AX646083.1 GI:28798462
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.

TITLE Guanine triphosphate-binding protein coupled receptors
JOURNAL Patent: EP 1270724-A 275 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP); Center for Advanced Science and Technology Incubation, Ltd.
(JP)

FEATURES Location/Qualifiers
source 1..1351
/organism="Homo sapiens"

CDS

/mol_type="unassigned DNA"
/db_xref="taxon:9606"
201..1151
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD69177.1"
/db_xref="GI:28798463"
/translation="MELWNFTLSGFTLVGILNDSGPELLCATITLILALISNGL
LILATMEARLHMPMYLLIGQLSIMDLFTSVVTPKALADLRENTISGGALOWF
LALTMGAEDELILAFAAYDRYVAI CHPLTYMTLMSRAQWIMVATSMILASLALIT
VYTMHVPFGRAOEIRHLICEI PHILKVAADTSRYELMVYMGVTFELPSLALILASY
TOLLITLHNPSEGRKALVTCSHLLVGMFYGATPMYVLPSSFSHSTRDNIIISV
FYIVTVALNPLIYLSLNKEMRLRLRVLGKMYLPAHSTL"

ORIGIN

Query Match 12.3%; Score 120; DB 6; Length 1351;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAATCATCTCTGTTTCTACACAAATGTCACTCCAGCCCTGAATCCACTCAT 885
DB 1007 ACAAGACAATCATCTCTGTTTCTACACAAATGTCACTCCAGCCCTGAATCCACTCAT 1066
QY 886 CTACAGCCTGAGGAATAGAGGTCAATGCGGCGCTTGAGAGAGGCTCTGGGAAAATACAT 945
DB 1067 CTACAGCCTGAGGAATAGAGGTCAATGCGGCGCTTGAGAGAGGCTCTGGGAAAATACAT 1126

Search completed: October 6, 2004, 04:56:59
Job time : 3868 secs

...hypertension, atherosclerosis, diabetes, or disorders related to cell signal processing.

PS Claim 8; Page 10; 111pp; English.

XX The present sequence is that of a nucleic acid encoding a novel human G-
 CC protein coupled receptor, designated GPCR1, that has structural and
 CC physiological functions characteristic of the olfactory receptor family.
 CC The invention provides GPCR1 polypeptides, nucleic acids and antibodies.
 CC These are useful for treating or preventing a GPCR1-associated disorder,
 CC such as cardiomyopathy, atherosclerosis, diabetes, or a disorder related
 CC to cell signal processing or metabolic pathway modulation in humans
 CC (claimed). They may further be used for treating or preventing e.g.
 CC developmental diseases, metabolic pathway disorders, retinal disorders,
 CC wasting disorders associated with chronic diseases, pain, cancer,
 CC psychiatric and neurological disorders (e.g. anxiety or schizophrenia),
 CC autoimmune diseases, allergies, bacterial, fungal, protozoal and viral
 CC infections, neurodegenerative diseases (e.g. Alzheimer's disease), and
 CC haematopoietic diseases. The proteins and nucleic acids may also be used
 CC as research tools, as diagnostic or prognostic markers, in gene therapy,
 CC for promoting tissue regeneration in vitro and in vivo, and as biological
 CC defence weapons. The nucleic acids may also be used in chromosome
 CC mapping, in tissue typing, in forensic biology (e.g. to identify
 CC individuals from minute biological samples), in forensic identification
 CC of a biological sample, as surrogate markers, and in pharmacogenomics

XX Sequence 977 BP; 215 A; 279 C; 220 G; 263 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 977; DB 6; Length 977;

XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACATAAAAAACATCATGAGAGTCCGGAATCCACCTTGGAGAGGCGCTCATCTT 60
 DB 1 GCACATAAAAAACATCATGAGAGTCCGGAATCCACCTTGGAGAGGCGCTCATCTT 60
 QY 61 GGTGGGAGTTCTGATGAGAGTGGGCTCTGAACTGCTCTATGCTATTTAAATCTT 120
 DB 61 GGTGGGAGTTCTGATGAGAGTGGGCTCTGAACTGCTCTATGCTATTTAAATCTT 120
 QY 121 ATACATGTTGGCACTGACGAGCATGTTCTGCTCTGCTGGCCATACATGAAAGCCG 180
 DB 121 ATACATGTTGGCACTGACGAGCATGTTCTGCTCTGCTGGCCATACATGAAAGCCG 180
 QY 181 GCTCCACATGCCCATGTAATCTCTGCTTGGGAGCTCTCTCTATGAGACCTCTGTTAC 240
 DB 181 GCTCCACATGCCCATGTAATCTCTGCTTGGGAGCTCTCTCTATGAGACCTCTGTTAC 240
 QY 241 ATCTGTTGACCTCCCAAGGCTTGGGAGCTTCTGCGAGAGAAACATATCTCTT 300
 DB 241 ATCTGTTGACCTCCCAAGGCTTGGGAGCTTCTGCGAGAGAAACATATCTCTT 300
 QY 301 TGGAGGCTGTCACATTCAGATGTTCTGCGACATGACATGAGGCTGAGACCTCCCT 360
 DB 301 TGGAGGCTGTCACATTCAGATGTTCTGCGACATGACATGAGGCTGAGACCTCCCT 360
 QY 361 ACTGGCTTATGAGCTGATGACAGTATGAGGCTATGCTATGCTGTAATATCATGAC 420
 DB 361 ACTGGCTTATGAGCTGATGACAGTATGAGGCTATGCTATGCTGTAATATCATGAC 420
 QY 421 CCTCATGAGCCCAAGAGTCTGCTGATCATGATGAGGCTGATGCTGATGCTGCT 480
 DB 421 CCTCATGAGCCCAAGAGTCTGCTGATCATGATGAGGCTGATGCTGATGCTGCT 480
 QY 481 GATTGCTATAGACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 481 GATTGCTATAGACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 541 CAGGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 CAGGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 601 GTATGAGCTTAT 660
 DB 601 GTATGAGCTTAT 660

QY 661 TGTGGCTCTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 661 TGTGGCTCTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 721 GAGGAGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 GAGGAGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 TGGCAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 TGGCAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 CTCTGTTTTCACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 CTCTGTTTTCACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 TAAAGAGTCAATGAGGAGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAG 960
 DB 901 TAAAGAGTCAATGAGGAGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAG 960
 QY 961 CAGGCTCTAGGAGAGA 977
 DB 961 CAGGCTCTAGGAGAGA 977

RESULT 2

AAH31857
 ID AAH31857 standard; DNA; 947 BP.

XX AAH31857;

DT 30-JUN-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 430.

KW Human; olfactory receptor; OR; primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

KW scent profile; scent fingerprint; scent representation; de.

OS Homo sapiens.

PN WO200127158-A2.

PN 19-APR-2001.

PE 06-OCT-2000; 2000WO-US027582.

PR 08-OCT-1999; 99US-0158615P.

PR 24-FEB-2000; 2000US-0184809P.

PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX WPI; 2001-290713/30.

DR New polynucleotides which encode polypeptides involved in olfactory

XX sensation for identifying olfactory agonists and antagonists.

PT Claim 8; Page 352; 1857pp; English.

PS The present sequence is one of a number of isolated polynucleotides which

XX encode polypeptides involved in olfactory sensation. The polynucleotides

CC can be used in screening for olfactory agonists and antagonists. The

CC methods allow for the determination of primary scents and the

CC identification of the odour receptors used to detect these primary

CC scents. The methods also enable determination of secondary scents and the

CC identification of combinations of odour receptors that are involved in

CC detecting such secondary scents. This enables the construction of a scent

CC representation (also called a scent fingerprint or scent profile), which

CC may be used to re-create and edit scents. Libraries of olfactory

CC receptors are useful for determining the interaction pattern of a

25-JAN-2002 (first entry)
DNA encoding G-protein coupled receptor (GCRC) #18.
G-protein coupled receptor; GCRC; vaccine; gene therapy;
cell proliferation disorder; cancer; arteriosclerosis disorder;
neurological disorder; epilepsy; stroke; cardiovascular disorder;
hypertension; ischaemic heart disease; gastrointestinal disorder;
anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
schizophrenic disorder; neuroskeletal disorder; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 1..951
/*tag= a
/product= "GCRC 18"
/note= "G-protein coupled receptor 18"
WO20016742-A2.
13-SEP-2001.
01-MAR-2001; 2001WO-US006814.
03-MAR-2000; 2000US-0186854P.
10-MAR-2000; 2000US-0188384P.
17-MAR-2000; 2000US-0190453P.
20-MAR-2000; 2000US-0190730P.
(INCY-) INCYTE GENOMICS INC.
Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM:
Lu DAM, Yue H, Khan FA, Pollock JL, Au-Young J, Yang J, Harland L,
Walsh RF, Lo TP, Borowsky ML,
WPI, 2001-656776/75.
P-PsDB; AAU0317.
Novel G-protein coupled receptor polypeptides, for treating and
preventing autoimmune/inflammatory disorders, neurological disorders,
cell proliferative disorders, cardiovascular disorders and viral
infections.
Claim 5; Page 139-140; 141pp: English.
The invention describes a novel isolated polypeptide, selected from a
group of 21 G-protein coupled receptor polypeptides (GCRC) and useful in
vaccines and gene therapy. The polypeptide (I) is useful for screening
for agonist or antagonist of (I), compounds specifically binding to (I),
or compounds that modulate the activity of (I). The polynucleotide
encoding (I) is useful for screening a compound for effectiveness in
altering expression of a target polynucleotide comprising (II), by
expressing a sample comprising the target polynucleotide to a compound,
detecting altered expression of the target polynucleotide, and comparing
the expression of the target polynucleotide in the presence of varying
amounts of compound and in the absence of the compound. (I) and (II) are
useful for diagnosis, treatment and prevention of cell proliferative
disorders (e.g. cancer, arteriosclerosis, atherosclerosis), neurological
disorders (e.g. epilepsy, stroke, schizophrenic disorders and
neuroskeletal disorders), gastrointestinal disorders (e.g. anorexia,
ischaemic heart disease), gastrointestinal disorders (e.g. diabetes mellitus,
peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
osteoporosis, psoriasis), and metabolic disorders such as obesity.
Furthermore, the polynucleotide is useful; as primers for detecting
single nucleotide polymorphisms; as elements in microarray, to monitor
expression profiles; to generate a transcript image of a tissue or cell
type, and to generate hybridisation probes useful in mapping the
naturally occurring genomic sequence. This sequence encodes G-protein
coupled receptor 18, one of 21 GCRC proteins described in the method of
the invention

XX	Sequence	951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;	
XX	Query Match	12.3%; Score 120; DB 5; Length 951;	
XX	Best Local Similarity	100.0%; Pred. No. 3.2e-49;	
XX	Matches 120; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY			
DB	826	ACAAGACACATCATCTCTGTTTCTTACACAAATTGTCACTCCAGCCTGAATCCACATCAT	885
OY	807	ACAAGACACATCATCTCTGTTTCTTACACAAATTGTCACTCCAGCCTGAATCCACATCAT	866
OY	886	CTAAGCCTGAGGAATTAAGAGGTCATGCGGAGCCTTAGAGAGGTCCTGGAAAATACAT	945
DB	867	CTACAGCCTGAGGAATTAAGAGGTCATGCGGAGCCTTAGAGAGGTCCTGGAAAATACAT	926
XX			
XX	RESULT 5		
XX	AAS42307	standard; cDNA; 951 BP.	
XX	AAS42307;		
XX	18-DEC-2001	(first entry)	
XX			
DE	Human cDNA encoding olfactory receptor AOLFRL07.		
XX	Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;		
KW	ss; food additive; cosmetic; fragrance; pharmaceutical additive.		
XX	Homo sapiens.		
XX	WO200168805-A2.		
XX			
XX	20-SEP-2001.		
XX			
XX	13-MAR-2001; 2001WO-US007771.		
XX			
PR	13-MAR-2000; 2000US-0188914P.		
PR	24-MAR-2000; 2000US-0192033P.		
PR	12-APR-2000; 2000US-0198474P.		
PR	24-APR-2000; 2000US-0199335P.		
PR	26-MAY-2000; 2000US-0207702P.		
PR	23-JUN-2000; 2000US-0213849P.		
PR	16-AUG-2000; 2000US-0226534P.		
PR	07-SEP-2000; 2000US-0230732P.		
PR	07-FEB-2001; 2001US-0266862P.		
XX			
PA	(SENO-) SENOMYX INC.		
XX			
PI	Zozulya S;		
XX			
DR	WPI; 2001-570867/64.		
DR	P-PSDS; AA024614.		
XX			
PT	Nucleic acids encoding human olfactory G protein-coupled receptors,		
PT	useful for screening for compounds involved in olfactory sensation,		
PT	the compounds can be used in the food, pharmaceutical and cosmetic		
PT	industries to customize odors.		
XX			
PS	Claim 1; Page 128; 319pp; English.		
XX			
CC	The invention relates to nucleic acids encoding human olfactory		
CC	receptors, OR, (a G protein-coupled receptor, GPCR). The OR's		
CC	specifically recognise molecules, odourants, that elicit specific		
CC	olfactory sensation. The human olfactory receptors and polynucleotides		
CC	encoding them are useful for screening a library of chemical compounds		
CC	for compounds that are involved in olfactory sensation. Modulators of		
CC	their activity are useful for pharmacological and genetic modulation of		
CC	olfactory signalling pathways. Therefore, they can be used in the food,		
CC	pharmaceutical and cosmetic industries to customise odours and		
CC	fragrances. The present sequence encodes a human olfactory receptor of		
CC	the invention		

SQ Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

Query Match

12.3%; Score 120; DB 5; Length 951;

Best Local Similarity 100.0%; Pred. No. 3.2e-49;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 826 ACAGAGCAACATCATCTGTTTCTACACAATTGTCACCTCAGCCCTGAATTCATCAT 885

DB 807 ACAGAGCAACATCATCTGTTTCTACACAATTGTCACCTCAGCCCTGAATTCATCAT 866

DY 886 CTACAGCCTGAGAGAAATTAAGAGGTCAATGCGGCTTGAAGAGGCTCTGGAAAAATACAT 945

DB 867 CTACAGCCTGAGAGAAATTAAGAGGTCAATGCGGCTTGAAGAGGCTCTGGAAAAATACAT 926

RESULT 6

AB243126
ID AB243126 standard; DNA; 951 BP.

AC AB243126;

DT 06-MAR-2003 (first entry)

DE Human GPCR polynucleotide SEQ ID NO 513.

KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;

KW drug development; gustatory; taste; fragrance; gene; ds.

OS Homo sapiens.

PN WO200216548-A2.

PD 28-FEB-2002.

PF 30-JUL-2001; 2001WO-IB001446.

PR 04-AUG-2000; 2000JP-00237818.

PR 13-FEB-2001; 2001JP-00034434.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Haga T, Takeda S, Mitaku S;

DR WPI; 2002-304118/34.

DR P-PSDB; ABP95852.

PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.

PS Claim 9; SEQ ID NO 513; 97bp + Sequence Listing; Japanese.

CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIFO at ftp.wifo.int/pub/published_pct_sequences

SQ Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

Query Match

12.3%; Score 120; DB 6; Length 951;

Best Local Similarity 100.0%; Pred. No. 3.2e-49;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 826 ACAGAGCAACATCATCTGTTTCTACACAATTGTCACCTCAGCCCTGAATTCATCAT 885

DB 807 ACAGAGCAACATCATCTGTTTCTACACAATTGTCACCTCAGCCCTGAATTCATCAT 866

DY 886 CTACAGCCTGAGAGAAATTAAGAGGTCAATGCGGCTTGAAGAGGCTCTGGAAAAATACAT 945

DB 867 CTACAGCCTGAGAGAAATTAAGAGGTCAATGCGGCTTGAAGAGGCTCTGGAAAAATACAT 926

RESULT 7

ABK68461

ID ABK68461 standard; DNA; 951 BP.

AC ABK68461;

DT 02-JUL-2002 (first entry)

DE Human DNA for olfactory and pheromone G protein-coupled receptor #61.

KW Human; ds; gene; olfactory and pheromone G protein coupled receptor;

KW GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;

KW anorectic; taste; fragrance; food additive; cosmetic; cell migration;

KW sterility; psychotic disorder; neurological disorder; anxiety;

KW schizophrenia; manic depression; depression; axonal growth;

KW menstrual cycle; appetite sexual motivation; sexual attraction;

KW aggression.

OS Homo sapiens.

PN WO200224726-A2.

PD 28-MAR-2002.

PF 21-SEP-2001; 2001WO-BE000162.

PR 22-SEP-2000; 2000EP-00870211.

PA (CHEM-) CHEMCOM SA.

PI Veithen A;

DR WPI; 2002-330013/36.

DR P-PSDB; AAU95574.

PT Novel pheromone G-protein coupled receptor and receptor-derived agonists,
PT antagonists or inhibitors useful in food or cosmetic products or in the
PT treatment or prevention of neurological disorders such as anxiety and
PT schizophrenia.

PS Disclosure, Page 196-197; 833bp; English.

CC The invention relates to olfactory and Pheromone G-protein coupled
CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
CC portion and its encoding polynucleotide. Also included are an agonist,
CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
CC comprising the polynucleotide, a cell transformed by the vector, a non-
CC human mammal comprising a partial or total deletion of the polynucleotide
CC encoding the receptor and screening (detection and possibly, recovering)
CC of compounds which are known or not known to be agonist, antagonists or
CC inhibitors of natural compounds to the GPCR. The receptor-derived
CC agonists, antagonists, inhibitors or compounds are used as an
CC improvement, elimination or substitution of an existing taste and/or a
CC fragrance of (or in) the food and/or cosmetic products. They can also be
CC used in the preparation of medicament in the treatment and/or prevention
CC of a mammalian disorder, such as cell migration, sterility, psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, depression, for promoting axonal growth, nerve cell
CC connection and nerve regeneration for modulating male and female
CC endocrine functions, hormone production and the menstrual cycle, for the
CC prevention or the treatment by stimulation of several mammalian
CC behaviours, such as stimulation or suppression of appetite, sexual
CC motivation, sexual attraction, aggression and for promoting or
CC suppressing chemical communication between organisms. The present
CC sequence is a human DNA encoding an olfactory and pheromone GPCR

SQ Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;
Query Match 12.3%; Score 120; DB 6; Length 951;
Best Local Similarity 100.0%; Pred. No. 3.2e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 826 ACAAGACACATCATCTCTGTTTCTACACAAATTGTCACTCCAGCCCTGAATCCATCAT 885
DB 807 ACAAGACACATCATCTCTGTTTCTACACAAATTGTCACTCCAGCCCTGAATCCATCAT 866
QY 886 CTACAGCCTGAGGAAATAGAGGATCATGCGGCGCTTGAGAGGGGTCTCGGAAAAATACAT 945
DB 867 CTACAGCCTGAGGAAATAGAGGATCATGCGGCGCTTGAGAGGGGTCTCGGAAAAATACAT 926

RESULT 8
ABK37593
ID ABK37593 standard; cDNA; 951 BP.
XX
AC ABK37593;
XX
DT 08-MAY-2002 (first entry)
XX
DE DNA encoding G-coupled olfactory receptor #95.
XX
KW Human; olfactory G-coupled receptor; sensory perception of odourant;
KW odour composition; taste composition; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200198526-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020122.
XX
PR 22-JUN-2000; 2000US-0213812P.
PR 13-MAR-2001; 2001US-00804291.
XX
PA (SENSO-) SENOMYX INC.
XX
PI Zozulya S, Stryer L;
XX
DR WPI; 2002-083330/11.
DR P-PSDB; AAU85234.
XX
PT Representing sensory perception of one or more odourants for the
PT identification and design of tastes and odors comprises providing a
PT representative group of n olfactory receptors.
XX
PS Example; Page 101; 182pp; English.
XX
SS The invention relates to a method of representing sensory perception of
CC one or more odourants. The method comprises: (a) providing a
CC representative class of n olfactory receptors or ligand binding domains
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of
CC at least one activity of one or more odourants selected from: (i) binding
CC one or more odourants to the LBD of at least one of the n olfactory
CC receptors; (ii) activating at least one of the n olfactory receptors with
CC the one or more odourants; and (iii) blocking at least one of the n
CC olfactory receptors with the one or more odourants; and (c) generating a
CC representation of sensory perception from the values X1 to Xn. The
CC representation of the sensory perception of odourants is useful for the
CC design and formulation of odour and taste compositions. ABK37499-ABK37754
CC and ABK37918-ABK37921 represent human olfactory G-coupled receptor coding
CC sequences and related PCR primers of the invention
XX
SQ Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;
Query Match 12.3%; Score 120; DB 6; Length 951;
Best Local Similarity 100.0%; Pred. No. 3.2e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACACATCATCTCTGTTTCTACACAAATTGTCACTCCAGCCCTGAATCCATCAT 885
DB 807 ACAAGACACATCATCTCTGTTTCTACACAAATTGTCACTCCAGCCCTGAATCCATCAT 866
QY 886 CTACAGCCTGAGGAAATAGAGGATCATGCGGCGCTTGAGAGGGGTCTCGGAAAAATACAT 945
DB 867 CTACAGCCTGAGGAAATAGAGGATCATGCGGCGCTTGAGAGGGGTCTCGGAAAAATACAT 926

RESULT 9
AAS11688
ID AAS11688 standard; DNA; 1008 BP.
XX
AC AAS11688;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human odorant receptor (OR) DNA #5.
XX
DE Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
KW GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytostatic; ds;
KW neurotropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
KW antinflammatory; odorant receptor; olfactory loss; trauma; HIV;
KW human immunodeficiency virus; neoplastic growth; neurological disorder;
KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
KW wound healing; asthma; Albright hereditary osteodystrophy;
KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
XX
OS Homo sapiens.
XX
PN WO200157215-A2.
XX
PD 09-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003923.
XX
PR 07-FEB-2000; 2000US-0180511P.
PR 07-FEB-2000; 2000US-0180630P.
PR 07-FEB-2000; 2000US-0180646P.
PR 08-FEB-2000; 2000US-0180930P.
PR 08-FEB-2000; 2000US-0181004P.
PR 08-FEB-2000; 2000US-0181013P.
PR 08-FEB-2000; 2000US-0181043P.
PR 24-JUL-2000; 2000US-0220594P.
PR 25-JUL-2000; 2000US-0224596P.
PR 11-AUG-2000; 2000US-0245292P.
PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
XX Baumgartner JC;
XX WPI; 2001-488883/53.
XX P-PSDB; AAU07088.
XX
PT Novel isolated NOVX polypeptide related to human odorant receptor family
PT of G-protein coupled receptor superfamily of proteins useful for treating
PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
XX
PS Claim 9; Page 44; 199pp; English.
XX
SS Novel isolated NOVX polynucleotides and their encoded polypeptides of the
CC invention are related to the human olfactory (or odorant) receptors
CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
CC sequences are useful for treating or preventing a pathology associated
CC with OR in a subject, and for manufacturing a medicament for treating a

CC syndrome associated with a human disease. These diseases include
CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
CC growth, neurological disorders, such as Parkinson's disease and
CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
CC disease, multiple sclerosis, and Albritt hereditary osteodysplasia. The
CC polynucleotides and polypeptides are also useful, to identify proteins of
CC the same family, to screen for molecules which inhibit or enhance the
CC activity or function of olfactory receptors, to detect nasal epithelial
CC neuronal tissue, in production of transgenic plants and for the
CC development of new drug targets for various disorders. This sequence
CC represents DNA encoding a human OR protein

SO Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other;

Query Match 12.3%; Score 120; DB 5; Length 1008;
Best Local Similarity 100.0%; Pred. No. 3.2e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACATCATCTCTGTTTCTACACAAATGTCACCTCAGCCCTGAATTCACCTAT 885
DB 857 ACAAGACATCATCTCTGTTTCTACACAAATGTCACCTCAGCCCTGAATTCACCTAT 916
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAGAGAGGTCCTGGAAATATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAGAGAGGTCCTGGAAATATCAT 976

RESULT 10

ABK53096
ID ABK53096 standard; cDNA, 1008 BP.

AC ABK53096;

D7 15-AUG-2002 (first entry)

DE cDNA sequence encoding novel odourant receptor NOV6 protein.

KM NOV; odourant receptor; G protein coupled receptor; GPCR; trauma; HIV;

KW ss; gene; olfactory receptor; olfactory loss; neoplastic growth;

KM Parkinson's disease; Alzheimer's disease; neurological disorder;

OS Unidentified.

Key Location/Qualifiers

FT 27..1001

FT /*tag= a

FT /product= "NOV6 protein"

PN WO200236632-A2.

PD 10-MAY-2002.

PF 09-OCT-2001; 2001WO-US031744.

PR 02-NOV-2000; 2000US-0245292P.

PR 06-FEB-2001; 2001US-00777789.

PR 20-SEP-2001; 2001US-00245292.

PA (CUBA-) CUBAGEN CORP.

PI Alsbrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;

PI Spytek KA;

DR WPI: 2002-471499/50.

DR P-PSDB; AAU97927.

PT New isolated olfactory receptor-like polypeptide, NOVX, useful for

PT diagnosing, preventing or treating disorders of olfactory loss, e.g.

PT trauma, human immunodeficiency virus illness, neoplastic growth and

XX neurological disorders.

PS Claim 9; Page 33; 122pp; English.

XX This invention relates to the DNA and protein sequences of a novel
CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC sequences of the invention and an antibody specific for the protein are
CC useful for treating or preventing a disorder associated with NOV1 in a
CC subject, preferably human. A NOVX specific antibody is useful for
CC determining the presence or amount of protein in a sample. The DNA,
CC protein and antibody of the invention is useful for diagnosing,
CC preventing or treating disorders associated with aberrant NOVX expression
CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC antibody is useful in screening assays, detection assays (e.g.,
CC medicine (e.g., diagnostic assays, prognostic assays), predictive
CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the cDNA encoding the NOV6 protein of the
CC invention

SO Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other;

Query Match 12.3%; Score 120; DB 6; Length 1008;
Best Local Similarity 100.0%; Pred. No. 3.2e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACATCATCTCTGTTTCTACACAAATGTCACCTCAGCCCTGAATTCACCTAT 885
DB 857 ACAAGACATCATCTCTGTTTCTACACAAATGTCACCTCAGCCCTGAATTCACCTAT 916
QY 886 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAGAGAGGTCCTGGAAATATCAT 945
DB 917 CTACAGCCTGAGGAATTAAGAGGTCATGCGGCGCTTGAGAGAGGTCCTGGAAATATCAT 976

RESULT 11

ABK53097
ID ABK53097 standard; cDNA, 1008 BP.

AC ABK53097;

D7 15-AUG-2002 (first entry)

DE cDNA sequence encoding novel odourant receptor NOV7 protein.

KM NOV; odourant receptor; G protein coupled receptor; GPCR; trauma; HIV;

KW ss; gene; olfactory receptor; olfactory loss; neoplastic growth;

KW human immunodeficiency virus; Alzheimer's disease; SNP;

OS Unidentified.

Key Location/Qualifiers

FT 27..1001

FT /*tag= a

FT /product= "NOV7 protein"

FT replace(278,T)

FT /tag= b

FT /standard_name= "Single nucleotide polymorphism"

PN WO200236632-A2.

PD 10-MAY-2002.

PF 09-OCT-2001; 2001WO-US031744.

PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
PR 20-SEP-2001; 2001US-00245292.

(CURA-) CURAGEN CORP.

Alcobrook JP, Burgess CE, Grosse WM, Lepley DM, Padgugan M,
 Spylek KA;
 WPI, 2002-47149/50.
 P-PSDB; AAU97928.

xx New isolated olfactory receptor-like polypeptide, NOX, useful for
 pt diagnosing, preventing or treating disorders of olfactory loss, e.g
 pt trauma, human immunodeficiency virus illness, neoplastic growth and
 pt neurological disorders.

Claim 9; Page 34; 122pp; English.

XX This invention relates to the DNA and protein sequences of a novel
CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC sequences of the invention and an antibody specific for the protein are
CC useful for treating or preventing a disorder associated with NOV1 in a
CC subject, preferably human. A NOVX specific antibody is useful for
CC determining the presence or amount of protein in a sample. The DNA,
CC protein and antibody of the invention is useful for diagnosing,
CC preventing or treating disorders associated with aberrant NOVX expression
CC such as disorders of olfactory loss, e.g., trauma, human immunodeficiency
CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.,
CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC antibody is useful in screening assays, detection assays (e.g.,
CC chromosomal mapping, tissue typing, forensic biology), predictive
CC medicine (e.g., diagnostic assays, prognostic assays), monitoring clinical
CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the cDNA encoding the NOV7 protein of the
CC invention.

Sequence 1008 BP; 216 A; 290 C; 234 G; 268 T; 0 U; 0 Other, SQ

Query Match 12.3%; Score 120; DB 6; Length 1008;

Best Local Similarity	100.0%	Pred. No. 3.2e-45
Matches 120: Conservative	0	Mismatches 0
Indels	0	Gaps 0

QY	826	ACAAACAACATCATCTCTGTTTTTTCACAAATTTGCATCCAGCCCTGAATCCATCAT	885
Db	857	ACAGACACATCATCTCTGTTTTTTCACAAATTTGCATCCAGCCCTGATCCATCAT	916
QY	886	CTACAGCCTGAGGAATPAGAGGTCATGCGGCGCTTGAGGAGGGTCTCTGGAAATATCAT	945
Db	917	CTACAGCCTGAGGAATPAGAGGTCATGCGGCGCTTGAGGAGGGTCTCTGGAAATATCAT	976

RESULT 12

AAS11687 standard; DNA; 1050 BP.

AC AAS11687;

DT 24-OCT-2001 (first entry)

Human odorant receptor (OR) DNA #4.

XX Human; olfactory receptor; OR; G-protein coupled receptor superfamily
KM GPCR; gene therapy; transducer; anti-HIV; cytostatic; ds
KM neurotrophic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
KM

KM anti-inflammatory; odorant receptor; olfactory loss; trauma; disorder;
 KM human immunodeficiency virus; neoplastic growth; neurological disorder;
 KM Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease
 KM wound healing; asthma; Alzheim hereditary osteodystrophy;
 KM multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
 XX
 OS Homo sapiens.

OS Homo sapiens

Key	Location/Qualification
PH	72.1022
FT	
CDS	

PN W0200157215-A2.

PD 09-AUG-2001

07-FEB-2001; 2001WO-US003923

PR 07-FEB-2000; 2000US-0180511P
PR 07-FEB-2000; 2000US-0180630P
PR 07-FEB-2000; 2000US-0180646P
PR 08-FEB-2000; 2000US-0180930P
PR 08-FEB-2000; 2000US-0181004P
PR 08-FEB-2000; 2000US-0181013P
PR 08-FEB-2000; 2000US-0181034P
PR 24-FEB-2000; 2000US-0220262P
PR 24-FEB-2000; 2000US-0220594P
PR 11-MAR-2000; 2000US-0224596P
PR 02-MAR-2000; 2000US-0245292P
PR 06-FEB-2001; 2001US-0077778P

PA (CURA-) CURAGEN CORP

XX Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS
PI Baumgartner JC;
PI

WPI; 2001-488883/53.
P-PSDB; AU07087.

XX Novel isolated NOVX polypeptide related to human odorant receptor family
PT of G-protein coupled receptor superfamily of proteins useful for treating
PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
XX
PS Claim 9; Page 39; 19pp; English.

XX Novel isolated NOXV polynucleotides and their encoded polypeptides of the
CC invention are related to the human olfactory (or odorant) receptors
CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
CC sequences are useful for treating or preventing a pathology associated
CC with OR in a subject, and for manufacturing a medicament for treating a
CC syndrome associated with a human disease. These diseases include
CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
CC disorders of olfactory loss, such as Parkinson's disease and
CC growth, neurological disorders, such as Alzheimer's disease, Crohn's
CC disease, multiple sclerosis, neurogenesis, cancer, wound healing, asthma, Crohn's
CC disease, multiple sclerosis, neurogenesis, cancer, wound healing, asthma, Crohn's
CC polynucleotides and polypeptides are also useful, to identify proteins of
CC the same family, to screen for molecules which inhibit or enhance the
CC activity or function of olfactory receptors, to detect nasal epithelial
CC neuronal tissue, in production of transgenic plants and for the
CC development of new drug targets for various disorders. This sequence
CC represents DNA encoding a human OR protein

XX	Sequence	1050 BP;	234 A;	293 C;	238 G;	285 T;	0 U;	0 Other
SQ								

Query Match	12.3%	Score 120;	DB 5;	Length 1050;
Best Local Similarity	100.0%;	Pred. No. 3.2e-49;		
Matches 120;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

QY 886 CTACAGCCTGAGGAATAGAGGATCATGCGGCGCTTGAGAGAGGCTTGGGAAATACAT 945
 DB 938 CTACAGCCTGAGGAATAGAGGATCATGCGGCGCTTGAGAGAGGCTTGGGAAATACAT 997

RESULT 13

ID ADC85822
 AC ADC85822 standard; DNA; 1351 BP.

XX
 AC ADC85822;

DT 01-JAN-2004 (first entry)

DE Human GPCR gene SEQ ID NO:275.

KW ds; gene; human; GPCR;

KM guanosine triphosphate-binding protein coupled receptor; gene therapy.

OS Homo sapiens.

FN EP1270724-A2.

PD 02-JAN-2003.

PF 18-JUN-2002; 2002EP-00013517.

PR 18-JUN-2001; 2001JP-00246789.

PA (NMAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

PI Suwa M, Asai K, Akiyama Y, Aburatani H;

DR WPI; 2003-315783/31.

DR P-PSDB; ADC85823.

PT New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.

PS Claim 1; SEQ ID NO 275; 28bp; English.

CC The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and CC polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the CC guanosine triphosphate-binding protein coupled receptor. The CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the CC invention.

SQ Sequence 1351 BP; 342 A; 340 C; 295 G; 374 T; 0 U; 0 Other;

Query Match 12.3%; Score 120; DB 9; Length 1351;
 Best Local Similarity 100.0%; Pred. No. 3.2e-49;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 826 ACAAGACAACATCATCTGTTTCTACCAATTGCACTCCAGCCCTGAATCACTCAT 885

DB 1007 ACAAGACAACATCATCTGTTTCTACCAATTGCACTCCAGCCCTGAATCACTCAT 1066

QY 886 CTACAGCCTGAGGAATAGAGGATCATGCGGCGCTTGAGAGAGGCTTGGGAAATACAT 945

DB 1067 CTACAGCCTGAGGAATAGAGGATCATGCGGCGCTTGAGAGAGGCTTGGGAAATACAT 1126

RESULT 14

ID AAA51192
 AC AAA51192 standard; CDNA; 678 BP.

AC AAA51192;

DT 26-SEP-2000 (first entry)

XX
 DE Murine olfactory receptor ligand-binding region cDNA 18.

KW Degenenerate primer, ligand-binding region; olfactory receptor;

KM Transmembrane domain; N-terminal; plasma membrane; translocation domain;

XX human rhodopsin receptor; odorant; toxicity; olfactory response; ss.

OS Mus musculus.

FN Key Location/Qualifiers

FT CDS 1..669

FT /*tag= a

FT /product= "Olfactory_receptor_ligand_binding_protein"

PN MO200035274-A1.

PD 22-JUN-2000.

PF 17-DEC-1999; 99WO-US030221.

PR 17-DEC-1998; 98US-00112605.

PA (UYO) UNITV JOHNS HOPKINS SCHOOL MEDICINE.

PI Reed RR, Krautwurst D, Yau KW;

DR WPI; 2000-431471/37.

DR P-PSDB; AA96679.

PT Primer pair for amplifying olfactory receptor nucleic acid, useful e.g. for producing receptor libraries used in e.g. screening odorants for toxicity.

PS Claim 18; Page 36-37; 61pp; English.

CC AAA51175-93 encode murine odorant/ligand binding regions of olfactory CC receptors. They were amplified using degenerate primers shown in AAA51163 CC -64. The primers can be used to generate a library of OR-LBR comprising CC the transmembrane domains (TMD) II-VI, III-VI, II-VII or III-VII. CC Chimeric nucleic acids encoding a 7-TMD protein comprise a sequence CC encoding an N-terminal plasma membrane translocation domain (especially CC the sequence shown in AA96658), a first TMD and the OR-LBR. The CC translocation domain was initially derived from the N-terminus of the CC human rhodopsin receptor. LBR produced by amplification with the primers CC are useful for generating new odorants, to screen for toxicity or CC therapeutic activity in odorants, and altering an animal's olfactory CC response (claimed)

SQ Sequence 678 BP; 148 A; 174 C; 119 G; 237 T; 0 U; 0 Other;

Query Match 2.8%; Score 27; DB 3; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.0069;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 CATGGCCTATGACAGGTATGTGCGCAT 396

DB 162 CATGGCCTATGACAGGTATGTGCGCAT 188

RESULT 15

ID ACA04914
 AC ACA04914 standard; CDNA; 678 BP.

AC ACA04914;

DT 28-MAY-2003 (first entry)

XX Mouse odorant/ligand binding region cDNA #18.

KW ss; olfactory receptor; odorant; ligand-binding region; mouse;

KM olfactory neuron; olfactory epithelium; 7 transmembrane receptor;

KM olfactory response.

```

XX OS Mus musculus.
XX PN US6492143-B1.
XX PD 10-DEC-2002.
XX PF 17-DEC-1999; 99US-00465901.
XX PR 17-DEC-1998; 98US-0112605P.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Reed RR, Yau K, Krautwurst D,
XX DR WPI: 2003-327314/31.
XX P-PSDB; AB067259.
XX PT Novel amplification primer sequence pair for amplifying nucleic acid
XX encoding an olfactory receptor ligand-binding region.
XX PS Example 1; Col 77-80; 46pp; English.
XX CC The invention relates to an amplification primer sequence pair for
XX amplifying a nucleic acid encoding an olfactory receptor ligand-binding
XX region, comprising a primers appearing as ACA04888 and ACA04889. Also
XX included is a kit for amplifying olfactory receptor sequences comprising
XX the primers. The primers are useful for generating a nucleic acid
XX sequence that encodes a ligand-binding region of an olfactory receptor.
XX The amplified nucleic acid is genomic DNA, mRNA or cDNA derived from
XX olfactory neurons or the olfactory epithelium. The olfactory receptors
XX are 7 transmembrane receptors, manipulation of which can modulate an
XX animal's olfactory response and can be used to generate novel odourants.
XX The present sequence encodes a mouse olfactory receptor ligand binding
XX region and is isolated using the primer of the invention
XX SQ Sequence 678 BP; 148 A; 174 C; 119 G; 237 T; 0 U; 0 Other;
XX
XX Query Match 2.8%; Score 27; DB 7; Length 678;
XX Best Local Similarity 100.0%; Pred. No. 0.0069;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 370 CATGCCCTATGACAGGTATGTGGCCAT 396
Db 162 CATGCCCTATGACAGGTATGTGGCCAT 188

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Search completed: October 6, 2004, 03:52:22
 Job time : 436 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
5315.559 Million cell updates/sec

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Perfect score: 977
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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size: 20

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	27	2.8	4	US-09-465-901-45
2	22	2.3	951	US-09-465-901-47
3	22	2.3	1320	US-08-599-252-84
4	22	2.3	1320	US-08-436-074-57
5	22	2.3	1320	PCT-US96-06352-84
6	22	2.3	1320	PCT-US96-06583-84
7	20	2.0	3383	US-08-884-324-12
8	20	2.0	11464	US-08-884-324-13
9	20	2.0	28994	US-08-884-324-14

ALIGNMENTS

RESULT 1
US-09-465-901-45
; Sequence 45, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-45

Query Match 2.8%; Score 27; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 CATGCCCTATGACAGGTATGTGGCCAT 396
DB 162 CATGCCCTATGACAGGTATGTGGCCAT 188

RESULT 2
US-09-465-901-47
; Sequence 47, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-47

Query Match 2.3%; Score 22; DB 4; Length 951;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 TGACAGGTATGTGGCCATTGT 400
DB 354 TGACAGGTATGTGGCCATTGT 375

RESULT 3
US-08-599-252-84/C
; Sequence 84, Application US/08599252
; Patent No. 5705343
; GENERAL INFORMATION:
; APPLICANT: DRAVNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GRIKKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; TITLE OF INVENTION: HEMOCHROMATOSIS
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,252
FILING DATE: 09-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-599-252-84

Query Match 2.3%; Score 22; DB 1; Length 1320;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 846 TTTTCTACACATGTGCTACTCC 867
DB 1210 TTTTCTACACATGTGCTACTCC 1189

RESULT 4
US-08-436-074-57/c
Sequence 57, Application US/08436074
Patent No. 5753438
GENERAL INFORMATION:
APPLICANT: DRAYNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GNIERKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,074
FILING DATE: 08-MAY-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-074-57

Query Match 2.3%; Score 22; DB 1; Length 1320;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 846 TTTTCTACACATGTGCTACTCC 867
DB 1210 TTTTCTACACATGTGCTACTCC 1189

RESULT 5
PCT-US96-06352-84/c
Sequence 84, Application PC/TUS9606352
GENERAL INFORMATION:
APPLICANT: DRAYNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GNIERKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESSES:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06352
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,252
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US96-06352-84

Query Match 2.3%; Score 22; DB 5; Length 1320;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 846 TTTTCTACACATGTGCTACTCC 867
|||||

Db 1210 TTTTCTACACATGTCTACTCC 1189

RESULT 6

PCT-US96-06583-84/c

Sequence 84, Application PC/TUS9606583

GENERAL INFORMATION:

APPLICANT: DRAVNA, DENNIS T.

APPLICANT: FEDER, JOHN N.

APPLICANT: GNIERKE, ANDREAS

APPLICANT: KIMMEL, BRUCE E.

APPLICANT: THOMAS, WINSTON J.

APPLICANT: WOLFE, ROGER K.

TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY

TITLE OF INVENTION: HEMOCHROMATOSIS

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/06583

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/599,252

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 9053-0001.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:

LENGTH: 1320 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US96-06583-84

Query Match

Best Local Similarity 2.3%; Score 22; DB 5; Length 1320;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 846 TTTTCTACACATGTCTACTCC 867

1210 TTTTCTACACATGTCTACTCC 1189

RESULT 7

US-08-884-324-12/c

Sequence 12, Application US/08884324

Patent No. 6060283

GENERAL INFORMATION:

APPLICANT: Takahori OKURA

APPLICANT: Kakuji TORIGOE

APPLICANT: Masahi KURIMOTO

TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE

OF INDUCING THE PRODUCTION OF INTERFERON-

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESSES:

ADDRESS: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/884,324

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 185,305/96

FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKURA=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 3383 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE:

ORGANISM: human

TISSUE TYPE: placenta

FEATURE:

NAME/KEY: Intron

LOCATION: 1..3383

IDENTIFICATION METHOD: E

US-08-884-324-12

Query Match

Best Local Similarity 2.0%; Score 20; DB 3; Length 3383;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 831 ACAACATCATCTCTGTTTC 850

2761 ACAACATCATCTCTGTTTC 2742

RESULT 8

US-08-884-324-13/c

Sequence 13, Application US/08884324

Patent No. 6060283

GENERAL INFORMATION:

APPLICANT: Takahori OKURA

APPLICANT: Kakuji TORIGOE

APPLICANT: Masahi KURIMOTO

TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE

OF INDUCING THE PRODUCTION OF INTERFERON-

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESSES:

ADDRESS: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11464 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..3
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 4..82
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 83..1453
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 1454..1465
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 1466..4848
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 4849..4865
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 4866..4983
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 4984..6317
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 6318..6451
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 6452..11224
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 11225..11443
IDENTIFICATION METHOD: S
NAME/KEY: 3'UTR
LOCATION: 11444..11464
IDENTIFICATION METHOD: E
US-08-884-324-13

Query Match 2.0%; Score 20; DB 3; Length 11464;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 831 ACAACATCATCTCTGTTTC 850
|||||
Db 4226 ACAACATCATCTGTTTC 4207

RESULT 9
US-08-884-324-14/c

Sequence 14, Application US/08884324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takamori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahiko KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..15606
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 15607..15685
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 15686..17056
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 17057..17068
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 17069..20451
IDENTIFICATION METHOD: E
NAME/KEY: leader peptide
LOCATION: 20452..20468
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 20469..20586
IDENTIFICATION METHOD: S
NAME/KEY: intron
LOCATION: 20587..21920
IDENTIFICATION METHOD: E
NAME/KEY: mat peptide
LOCATION: 21921..22054
IDENTIFICATION METHOD: S

```

; NAME/KEY: intron
; LOCATION: 22055..26827
; IDENTIFICATION METHOD: E
; NAME/KEY: mat peptide
; LOCATION: 26828..27046
; IDENTIFICATION METHOD: S
; NAME/KEY: 3'UTR
; LOCATION: 27047..28994
; IDENTIFICATION METHOD: E
US-08-884-324-14

```

```

Query Match      2.0%; Score 20; DB 3; Length 28994;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      831 ACAACATCATCTGTGTTTC 850
          |||||
Db      19829 ACAACATCATCTGTGTTTC 19810

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Search completed: October 6, 2004, 05:40:52
 Job time : 102 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 14:09:13 ; Search time 122 Seconds

(without alignments)
731.844 Million cell updates/sec

Title: US-10-024-444B-2

Perfect score: 316

Sequence: 1 MELNSTLGSGLIVGLIND.....VMRALRVLYKTYILAHSTL 316

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1586107 segs, 282547505 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	316	100.0	316	4	AAg71681 Human Olf
2	316	100.0	316	5	ABb79908 Human Olf
3	57	18.0	316	4	AAg71678 Human Olf
4	57	18.0	316	4	AAU10317 G-protein
5	57	18.0	316	4	AAU24614 Human Olf
6	57	18.0	316	4	AAU07087 Human Olf
7	57	18.0	316	5	ABp95852 Human GPC
8	57	18.0	316	5	AAU95574 Human Olf
9	57	18.0	316	7	ADc85823 G-coupled
10	57	18.0	324	4	AAU97088 Human odo
11	57	18.0	324	5	AAU97928 Novel odo
12	57	18.0	324	5	AAU97927 Novel odo
13	57	18.0	324	4	AAg73027 Olfactory
14	57	18.0	316	5	AAg71196 Human GPC
15	57	18.0	316	7	ADD12793 Novel hum
16	57	18.0	316	4	AAg72581 Murine OR
17	57	18.0	316	4	AAg71586 Human Olf
18	57	18.0	316	4	AAg71586 Human Olf
19	57	18.0	316	4	AAg71586 Human Olf
20	57	18.0	316	4	AAg71586 Human Olf
21	57	18.0	316	4	AAg71586 Human Olf
22	57	18.0	316	4	AAg71586 Human Olf
23	57	18.0	316	4	AAg71586 Human Olf
24	57	18.0	316	4	AAg71586 Human Olf
25	57	18.0	316	4	AAg71586 Human Olf

26	14	4.4	317	5	AAU95552 Human Olf
27	14	4.4	317	5	AAU85236 G-coupled
28	14	4.4	317	7	ADc86213 Human GPC
29	13	4.1	82	4	AAb45704 Human 7TM
30	13	4.1	149	3	AAb41578 Human ORF
31	13	4.1	158	7	ADc86807 Human GPC
32	13	4.1	172	7	ADc86715 Human GPC
33	13	4.1	199	7	ADc86715 Human GPC
34	13	4.1	202	4	AAg71547 Human Olf
35	13	4.1	210	4	AAg72738 Human Olf
36	13	4.1	211	4	AAg72737 Human Olf
37	13	4.1	212	2	AAg72737 Human Olf
38	13	4.1	215	4	AAg72749 Human Olf
39	13	4.1	216	4	AAg72799 Human Olf
40	13	4.1	216	4	AAg71988 Human Olf
41	13	4.1	216	4	AAg72796 Human Olf
42	13	4.1	216	4	AAg72336 Human OR-
43	13	4.1	216	4	AAg72842 Human Olf
44	13	4.1	216	4	AAg72797 Human Olf
45	13	4.1	216	4	AAg72786 Human Olf

ALIGNMENTS

RESULT 1
ID AAg71681 standard; protein; 316 AA.
AC AAg71681;
DT 30-JUL-2001 (first entry)
DE Human olfactory receptor polypeptide, SEQ ID NO: 1362.
KW Human, olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
OS Homo sapiens.
PN WO200127158-A2.
PD 19-APR-2001.
PE 06-OCT-2000; 2000WO-US027582.
PF 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
PA (DIGT-) DIGSCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
DR WPI; 2001-290713/30.
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
PS Claim 11; Page 845; 1857BP; English.
XX The present sequence is an olfactory receptor which is encoded by one of
XX a number of novel polynucleotides. The polynucleotides can be used in
XX screening for olfactory agonists and antagonists. The methods allow for
XX the determination of primary scents and the identification of the odour
XX receptors used to detect these primary scents. The methods also enable
XX determination of secondary scents and the identification of combinations
XX of odour receptors that are involved in detecting such secondary scents.
XX This enables the construction of a scent representation (also called a
XX scent fingerprint or scent profile), which may be used to re-create and
XX edit scents. Libraries of olfactory receptors are useful for determining
XX the interaction pattern of a composition with the receptors, and can be

KM scent profile; scent fingerprint; scent representation.
 XX
 OS Homo sapiens.
 XX
 FN WO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US027582.
 XX
 PR 08-OCT-1999; 99US-0158615P.
 PR 24-FEB-2000; 2000US-0184809P.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Beljenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX
 DR WPI; 2001-290713/30.
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 PS
 PS Claim 11; Page 842-843; 1857pp; English.
 XX
 CC The present sequence is an olfactory receptor which is encoded by one of
 CC a number of novel polynucleotides. The polynucleotides can be used in
 CC screening for olfactory agonists and antagonists. The methods allow for
 CC the determination of primary scents and the identification of the odor
 CC receptors used to detect these primary scents. The methods also enable
 CC determination of secondary scents and the identification of combinations
 CC of odor receptors that are involved in detecting such secondary scents.
 CC This enables the construction of a scent representation (also called a
 CC scent fingerprint or scent profile), which may be used to re-create and
 CC edit scents. Libraries of olfactory receptors are useful for determining
 CC the interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals
 CC
 XX
 SQ Sequence 316 AA;
 Query Match 18.0%; Score 57; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 EARLHMPMYLLGQLSLMDLLFTSVTPPKALADFLRRENTISFGGCAQMFALTMG 108
 DB 52 EARLHMPMYLLGQLSLMDLLFTSVTPPKALADFLRRENTISFGGCAQMFALTMG 108
 RESULT 4
 ID AAU10317 standard; protein; 316 AA.
 XX
 AC AAU10317;
 XX
 DT 25-JAN-2002 (first entry)
 XX
 DE G-protein coupled receptor (GPCR) #18.
 XX
 DE G-protein coupled receptor; GPCR; vaccine; gene therapy;
 KM cell proliferation disorder; epilepsy; stroke; cardiovascular disorder;
 KM neurological disorder; epilepsy; stroke; cardiovascular disorder;
 KM hypertension; ischemic heart disease; gastrointestinal disorder;
 KM anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
 KM diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
 KM schizophrenia disorder; neuroskeletal disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200166742-A2.
 XX
 PD 13-SEP-2001.

XX
 PF 01-MAR-2001; 2001WO-US006814.
 XX
 PR 03-MAR-2000; 2000US-0186854P.
 PR 10-MAR-2000; 2000US-0188384P.
 PR 17-MAR-2000; 2000US-0190453P.
 PR 20-MAR-2000; 2000US-0190730P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
 PI Lu DAM, Yue H, Khan PA, Policky JL, Au-Young J, Yang J, Harland L;
 PI Walsh RT, Lo TP, Borowsky ML;
 XX
 DR WPI; 2001-656776/75.
 DR N-PSDB; AASIS914.
 XX
 XX Novel G-protein coupled receptor polypeptides, for treating and
 PT preventing autoimmune/inflammatory disorders, neurological disorders,
 PT cell proliferative disorders, cardiovascular disorders and viral
 PT infections.
 PS
 PS Claim 1; Page 128; 141pp; English.
 XX
 CC The invention describes a novel isolated polypeptide, selected from a
 CC group of 21 G-protein coupled receptor polypeptides (GPCR) and useful in
 CC vaccines and gene therapy. The polypeptide (I) is useful for screening
 CC for agonist or antagonist of (I), compounds specifically binding to (I),
 CC or compounds that modulate the activity of (I). The polynucleotide
 CC encoding (I) is useful for screening a compound for effectiveness in
 CC altering expression of a target polynucleotide comprising (II), by
 CC exposing a sample comprising the target polynucleotide to a compound,
 CC detecting altered expression of the target polynucleotide, and comparing
 CC the expression of the target polynucleotide in the presence of varying
 CC amounts of compound and in the absence of the compound. (I) and (II) are
 CC useful for diagnosis, treatment and prevention of cell proliferative
 CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological
 CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
 CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
 CC ischemic heart disease), gastrointestinal disorders (e.g. anorexia,
 CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
 CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
 CC Furthermore, the polynucleotide is useful, as primers for detecting
 CC single nucleotide polymorphisms; as elements in microarray, to monitor or
 CC measure protein-protein interactions, drug-target interactions, and gene
 CC expression profiles; to generate a transcript image of a tissue or cell
 CC type, and to generate hybridisation probes useful in mapping the
 CC naturally occurring genomic sequence. This is the G-protein coupled
 CC receptor 18 (GPCR-18), one of 21 GPCR proteins described in the method
 CC of the invention
 CC
 XX
 SQ Sequence 316 AA;
 Query Match 18.0%; Score 57; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 EARLHMPMYLLGQLSLMDLLFTSVTPPKALADFLRRENTISFGGCAQMFALTMG 108
 DB 52 EARLHMPMYLLGQLSLMDLLFTSVTPPKALADFLRRENTISFGGCAQMFALTMG 108
 RESULT 5
 ID AAU24614 standard; protein; 316 AA.
 XX
 AC AAU24614;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human olfactory receptor AOUFR107.
 XX
 DE Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KM

KW food additive; cosmetic; fragrance; pharmaceutical additive.
 XX Homo sapiens.
 OS
 XX MO200168805-A2.
 PN
 XX 20-SEP-2001.
 PD
 XX 13-MAR-2001; 2001WO-US007771.
 PF
 XX 13-MAR-2001; 2000US-0188914P.
 PR 13-MAR-2001; 2000US-0192033P.
 PR 12-APR-2001; 2000US-0198474P.
 PR 24-APR-2001; 2000US-0199335P.
 PR 24-MAR-2001; 2000US-0207702P.
 PR 23-JUN-2001; 2000US-021849P.
 PR 16-AUG-2001; 2000US-0226534P.
 PR 07-SEP-2001; 2000US-0230732P.
 PR 07-FEB-2001; 2001US-0266862P.
 XX
 PA (SEMO-) SENOMTX INC.
 XX
 XX Zozulya S;
 XX
 XX WPI; 2001-570867/64.
 DR N-PSDB; AAS42307.
 DR
 XX Nucleic acids encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation, where
 PT the compounds can be used in the food, pharmaceutical and cosmetic
 PT industries to customize odors.
 PS
 XX Claim 60; Page 127; 319pp; English.
 CC The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor of the
 CC invention
 CC
 CC Sequence 316 AA;
 SQ
 QY Query Match 18.0%; Score 57; DB 4; Length 316;
 DB Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRRENTISFGGALQMFALTING 108
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRRENTISFGGALQMFALTING 108
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRRENTISFGGALQMFALTING 108
 ID AAU07087 standard; protein; 316 AA.
 AC AAU07087;
 XX
 XX 24-OCT-2001 (first entry)
 DT
 XX Human odorant receptor (OR) polypeptide #4.
 DE
 XX Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
 KW GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytostatic;
 KW neurotropic; neuroprotective; antiparkinsonian; antiallathmic; cancer;
 KW antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
 KW human immunodeficiency virus; neoplastic growth; neurological disorder;
 KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;

KW wound healing; asthma; Albright hereditary osteodystrophy;
 KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
 XX
 OS Homo sapiens.
 XX
 XX MO200157215-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 07-FEB-2001; 2001WO-US003923.
 PF
 XX 07-FEB-2001; 2000US-0180511P.
 PR 07-FEB-2001; 2000US-0180630P.
 PR 07-FEB-2001; 2000US-0180646P.
 PR 08-FEB-2001; 2000US-0180930P.
 PR 08-FEB-2001; 2000US-0181004P.
 PR 08-FEB-2001; 2000US-0181013P.
 PR 08-FEB-2001; 2000US-0181043P.
 PR 24-JUL-2001; 2000US-0220262P.
 PR 25-JUL-2001; 2000US-0220594P.
 PR 11-AUG-2001; 2000US-0224596P.
 PR 02-NOV-2001; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-00777789.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
 PI Baumgartner JC;
 PI WPI; 2001-488863/53.
 DR N-PSDB; AAS11687.
 DR
 XX Novel isolated NOVX polypeptide related to human odorant receptor family
 PT of G-protein coupled receptor superfamily of proteins useful for treating
 PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
 PS
 XX Claim 1; Page 39; 199pp; English.
 CC Novel isolated NOVX polynucleotides and their encoded polypeptides of the
 CC invention are related to the human olfactory (or odorant) receptors
 CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
 CC sequences are useful for treating or preventing a pathology associated
 CC with OR in a subject, and for manufacturing a medicament for treating a
 CC syndrome associated with a human disease. These diseases include
 CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
 CC growth, neurological disorders, such as Parkinson's disease and
 CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
 CC disease, multiple sclerosis, and Albright hereditary osteodystrophy. The
 CC polynucleotides and polypeptides are also useful, to identify proteins of
 CC the same family, to screen for molecules which inhibit or enhance the
 CC activity or function of olfactory receptors, to detect nasal epithelial
 CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents a human OR polypeptide
 CC
 CC Sequence 316 AA;
 SQ
 QY Query Match 18.0%; Score 57; DB 4; Length 316;
 DB Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRRENTISFGGALQMFALTING 108
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRRENTISFGGALQMFALTING 108
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRRENTISFGGALQMFALTING 108
 ID ABP95852 standard; protein; 316 AA.
 AC ABP95852;
 XX
 XX 06-MAR-2003 (first entry)
 DT

XX DE Human GPCR polypeptide SEQ ID NO 514.
 XX KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 XX KW drug development; gustatory; taste; fragrance; receptor.
 OS Homo sapiens.
 XX WO200216548-A2.
 XX PN 28-FEB-2002.
 XX PD 30-JUL-2001; 2001WO-1B001446.
 XX PF 04-AUG-2000; 2000JP-00237818.
 XX PR 13-FEB-2001; 2001JP-00034434.
 XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX HA Haga T, Takeda S, Mitaku S;
 XX DR WPI; 2002-304118/34.
 XX DR N-PSDB; ABZ43126.
 PT Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 PS Claim 10; SEQ ID NO 514; 97pp + Sequence Listing; Japanese.
 CC The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets for
 CC drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIP0 at ftp.wipo.int/pub/published_pcr_sequences
 XX SQ Sequence 316 AA;
 QY Query Match 18.0%; Score 57; DB 5; Length 316;
 Db Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRENTISFGGALOMFLATMG 108
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRENTISFGGALOMFLATMG 108
 RESULT 8
 AA095574 standard; protein; 316 AA.
 XX ID AA095574;
 XX AC AA095574;
 XX DT 02-JUL-2002 (first entry)
 XX DE Human olfactory and pheromone G protein-coupled receptor #61.
 XX KW Human; olfactory and pheromone G protein coupled; receptor; GPCR;
 XX KW tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
 XX KW anorectic; taste; fragrance; food additive; cosmetic; cell migration;
 XX KW sterility; psychotic disorder; neurological disorder; anxiety;
 XX KW schizophrenia; manic depression; depression; axonal growth;
 XX KW menstrual cycle; appetite sexual motivation; sexual attraction;
 XX KW aggression.
 OS Homo sapiens.

XX PN WO200224726-A2.
 XX XX 28-MAR-2002.
 XX PF 21-SEP-2001; 2001WO-BE000162.
 XX PR 22-SEP-2000; 2000EP-00870211.
 XX PA (CHEM-) CHEMCOM SA.
 XX VE Veichen A;
 XX DR WPI; 2002-330013/36.
 XX DR N-PSDB; ABK68461.
 PT Novel pheromone G-protein coupled receptor and receptor-derived agonists,
 PT antagonists or inhibitors useful in food or cosmetic products or in the
 PT treatment or prevention of neurological disorders such as anxiety and
 PT schizophrenia.
 PS Disclosure; Page 197-198; 833pp; English.
 CC The invention relates to olfactory and Pheromone G-protein coupled
 CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
 CC portion and its encoding polynucleotide. Also included are an agonist,
 CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
 CC comprising the polynucleotide, a cell transformed by the vector, a non-
 CC encoding the receptor and screening (detection and possibly, recovering)
 CC of compounds which are known or not known to be agonist, antagonists or
 CC inhibitors of natural compounds to the GPCR. The receptor-derived
 CC agonists, antagonists, inhibitors or compounds are used as an
 CC improvement, elimination or substitution of an existing taste and/or a
 CC fragrance of (or in) the food and/or cosmetic products. They can also be
 CC used in the preparation of medicament in the treatment and/or prevention
 CC of a mammalian disorder, such as cell migration, sterility, psychotic and
 CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, depression, for promoting axonal growth, nerve cell
 CC connection and nerve regeneration for modulating male and female
 CC endocrine functions, hormone production and the menstrual cycle, for the
 CC prevention or the treatment by stimulation of several mammalian
 CC behaviours, such as stimulation or suppression of appetite, sexual
 CC motivation, sexual attraction, aggression and for promoting or
 CC suppressing chemical communication between organisms. The present
 CC sequence is a human olfactory and pheromone GPCR protein sequence
 XX SQ Sequence 316 AA;
 QY Query Match 18.0%; Score 57; DB 5; Length 316;
 Db Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRENTISFGGALOMFLATMG 108
 52 EARLHMPYLLIGQLSIMDLFTSVTPKALADFLRENTISFGGALOMFLATMG 108
 RESULT 9
 AA085234 standard; protein; 316 AA.
 XX ID AA085234;
 XX AC AA085234;
 XX DT 08-MAY-2002 (first entry)
 XX DE G-coupled olfactory receptor #95.
 XX KW Human; olfactory G-coupled receptor; sensory perception of odourant;
 XX KW odour composition; taste composition.
 XX KW aggression.
 OS Homo sapiens.

PN WO200198526-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US020122.
 XX
 PR 22-JUN-2000; 2000US-0213812P.
 XX
 PR 13-MAR-2001; 2001US-00804291.
 XX
 PA (SENO-) SENOMYX INC.
 XX
 PI Zozulya S, Stryer L;
 XX
 DR WPI; 2002-083330/11.
 XX
 DR N-PSDB; ABK37593.
 XX
 PT Representing sensory perception of one or more odourants for the
 PT identification and design of tastes and odors comprises providing a
 PT representative group of n olfactory receptors.
 XX
 PS Claim 1; Page 101; 182pp; English.
 XX
 CC The invention relates to a method of representing sensory perception of
 CC one or more odourants. The method comprises: (a) providing a
 CC representative class of n olfactory receptors or ligand binding domains
 CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of
 CC at least one activity of one or more odourants selected from: (i) Binding
 CC one or more odourants to the LBD of at least one of the n olfactory
 CC receptors; (ii) activating at least one of the n olfactory receptors with
 CC the one or more odourants; and (iii) blocking at least one of the n
 CC olfactory receptors with the one or more odourants; and (c) generating a
 CC representation of the sensory perception from the values X1 to Xn. The
 CC representation of the sensory perception of odourants is useful for the
 CC design and formulation of odour and taste compositions. AA085140-AA085393
 CC represent human olfactory G-coupled receptor amino acid sequences of the
 CC invention
 XX
 SQ Sequence 316 AA;
 XX
 Query Match 18.0%; Score 57; DB 5; Length 316;
 Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 EARLHMPYLLIGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALATMG 108
 DB 52 EARLHMPYLLIGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALATMG 108
 XX
 RESULT 10
 ADC85823
 ID ADC85823 standard; protein; 316 AA.
 XX
 AC ADC85823;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DR Human GPCR protein SEQ ID NO:276.
 XX
 KM human; GPCR; guanosine triphosphate-binding protein coupled receptor;
 KM gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1270724-A2.
 XX
 PD 02-JAN-2003.
 XX
 PF 18-JUN-2002; 2002EP-00013517.
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;
 PI WPI; 2003-315783/31.
 XX
 DR N-PSDB; ADC85822.
 XX
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX
 PS Claim 2; SEQ ID NO 276; 28pp; English.
 XX
 CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The protein
 CC sequences shown in ADC8549-ADC87617 represent GPCR's of the invention.
 XX
 SQ Sequence 316 AA;
 XX
 Query Match 18.0%; Score 57; DB 7; Length 316;
 Best Local Similarity 100.0%; Pred. No. 9.3e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 EARLHMPYLLIGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALATMG 108
 DB 52 EARLHMPYLLIGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALATMG 108
 XX
 RESULT 11
 AAU07088
 ID AAU07088 standard; protein; 324 AA.
 XX
 AC AAU07088;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human odorant receptor (OR) polypeptide #5.
 XX
 KM Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
 KM GPCR; gene therapy; tranquiliser; vulnereary; anti-HIV; cyostatic;
 KM nociceptic; neuroprotective; antiparkinsonian; antisthmatic; cancer;
 KM antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
 KM human immunodeficiency virus; neoplastic growth; neurological disorder;
 KM Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
 KM wound healing; asthma; Albright hereditary osteodystrophy;
 KM multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
 XX
 OS Homo sapiens.
 XX
 PN WO200157215-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 07-FEB-2001; 2001WO-US003923.
 XX
 PR 07-FEB-2000; 2000US-0180511P.
 PR 07-FEB-2000; 2000US-0180630P.
 PR 07-FEB-2000; 2000US-0180646P.
 PR 08-FEB-2000; 2000US-0180930P.
 PR 08-FEB-2000; 2000US-0181004P.
 PR 08-FEB-2000; 2000US-0181013P.
 PR 08-FEB-2000; 2000US-0181043P.
 PR 24-JUL-2000; 2000US-0220262P.
 PR 24-JUL-2000; 2000US-0220594P.
 PR 25-JUL-2000; 2000US-0224596P.
 PR 11-AUG-2000; 2000US-0245232P.
 PR 02-NOV-2000; 2000US-0245232P.
 PR 06-FEB-2001; 2001US-00777789.
 XX
 PA (CURA-) CURAGEN CORP.

PI Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
 PI Baumgartner JC;
 XX
 DR WPI; 2001-48883/53.
 XX N-PSDB; AAS11688.
 XX
 PT Novel isolated NOXV polypeptide related to human odorant receptor family
 PT of G-protein coupled receptor superfamily of proteins useful for treating
 PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
 XX
 PS Claim 1; Page 44; 199pp; English.
 XX
 CC Novel isolated NOXV polynucleotides and their encoded polypeptides of the
 CC invention are related to the human olfactory (or odorant) receptors
 CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
 CC sequences are useful for treating or preventing a pathology associated
 CC with OR in a subject, and for manufacturing a medicament for treating a
 CC syndrome associated with a human disease. These diseases include
 CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
 CC growth, neurological disorders, such as Parkinson's disease and
 CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
 CC disease, multiple sclerosis, and Alibright hereditary osteodysplrophy. The
 CC polynucleotides and polypeptides are also useful, to identify proteins of
 CC the same family, to screen for molecules which inhibit or enhance the
 CC activity or function of olfactory receptors, to detect nasal epithelial
 CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents a human OR polypeptide
 XX
 SQ Sequence 324 AA;
 XX
 Query Match 18.0%; Score 57; DB 4; Length 324;
 Best Local Similarity 100.0%; Pred. No. 9.5e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 EARLHMPMYLLGQLSLMDLFTSVTPKALADFLRRENTISFGGCALOWFLATLTMG 108
 DB 60 EARLHMPMYLLGQLSLMDLFTSVTPKALADFLRRENTISFGGCALOWFLATLTMG 116
 XX
 RESULT 12
 AAU97928
 ID AAU97928 standard; protein; 324 AA.
 XX
 AC AAU97928;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Novel odorant receptor NOV7 protein.
 XX
 KM NOV; odorant receptor; G protein coupled receptor; GPCR; trauma;
 KM olfactory receptor; olfactory loss; neoplastic growth;
 KM human immunodeficiency virus; Alzheimer's disease; HIV;
 KM neurological disorder; Parkinson's disease.
 XX
 OS Unidentified.
 XX
 PN WO200236632-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 09-OCT-2001; 2001WO-US031744.
 XX
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-00777789.
 PR 20-SEP-2001; 2001US-00245292.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsbrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;
 PI Spytek KA;
 XX
 DR WPI; 2002-471499/50.

DR N-PSDB; ABK53097.
 XX
 XX New isolated olfactory receptor-like polypeptide, NOXV, useful for
 PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
 PT trauma, human immunodeficiency virus illness, neoplastic growth and
 PT neurological disorders.
 XX
 PS Claim 1; Page 34-35; 122pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of a novel
 CC isolated olfactory receptor-like polypeptide, NOXV. The DNA and protein
 CC sequences of the invention and an antibody specific for the protein are
 CC useful for treating or preventing a disorder associated with NOXV in a
 CC subject, preferably human. A NOXV specific antibody is useful for
 CC determining the presence or amount of protein in a sample. The DNA,
 CC protein and antibody of the invention is useful for diagnosing,
 CC preventing or treating disorders associated with aberrant NOXV expression
 CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
 CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
 CC Parkinson's disease and Alzheimer's disease. The sequences and NOX
 CC antibody is useful in screening assays, detection assays (e.g.,
 CC chromosomal mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
 CC trials and pharmacogenomic), and in methods of treatment (e.g.,
 CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
 CC produce antibodies immunospecific for the protein, to screen for
 CC potential agonist and antagonist compounds, and as bait protein in a two-
 CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
 CC therapy, to express the protein, to detect NOXV mRNA or a genetic lesion
 CC in a NOXV gene, and to modulate NOXV activity. The antibody of the
 CC invention is useful for isolating, and purifying the protein and to
 CC monitor protein levels in tissue as part of a clinical testing procedure.
 CC The present sequence represents the NOV protein of the invention
 XX
 SQ Sequence 324 AA;
 XX
 Query Match 18.0%; Score 57; DB 5; Length 324;
 Best Local Similarity 100.0%; Pred. No. 9.5e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 EARLHMPMYLLGQLSLMDLFTSVTPKALADFLRRENTISFGGCALOWFLATLTMG 108
 DB 60 EARLHMPMYLLGQLSLMDLFTSVTPKALADFLRRENTISFGGCALOWFLATLTMG 116
 XX
 RESULT 13
 AAU97927
 ID AAU97927 standard; protein; 324 AA.
 XX
 AC AAU97927;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Novel odorant receptor NOV6 protein.
 XX
 KM NOV; odorant receptor; G protein coupled receptor; GPCR; trauma;
 KM olfactory receptor; olfactory loss; neoplastic growth;
 KM human immunodeficiency virus; Alzheimer's disease; HIV;
 KM neurological disorder; Parkinson's disease.
 XX
 OS Unidentified.
 XX
 PN WO200236632-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 09-OCT-2001; 2001WO-US031744.
 XX
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-00777789.
 PR 20-SEP-2001; 2001US-00245292.
 XX
 PA (CURA-) CURAGEN CORP.
 XX

XX AIsobrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;
 PI Szytek KA;
 XX WPI, 2002-471499/50.
 DR N-PSDB; ABR3096.
 XX New isolated olfactory receptor-like polypeptide, NOVX, useful for
 PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
 PT trauma, human immunodeficiency virus illness, neoplastic growth and
 PT neurological disorders.
 XX
 PS Claim 1; Page 33; 122pp; English.
 CC This invention relates to the DNA and protein sequences of a novel
 CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
 CC sequences of the invention and an antibody specific for the protein are
 CC useful for treating or preventing a disorder associated with NOVX in a
 CC subject, preferably human. A NOVX specific antibody is useful for
 CC determining the presence or amount of protein in a sample. The DNA,
 CC protein and antibody of the invention is useful for diagnosing,
 CC preventing or treating disorders associated with aberrant NOVX expression
 CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
 CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
 CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
 CC antibody is useful in screening assays, detection assays (e.g.,
 CC chromosomal mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g., diagnostic assays, prognostic assays), monitoring clinical
 CC trials and pharmacogenomic), and in methods of treatment (e.g.,
 CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
 CC produce antibodies immunospecific for the protein, to screen for
 CC potential agonist and antagonist compounds, and as bait protein in a two-
 CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
 CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
 CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
 CC invention is useful for isolating, and purifying the protein and to
 CC monitor protein levels in tissue as part of a clinical testing procedure.
 CC The present sequence represents the NOV6 protein of the invention
 CC
 XX
 SQ Sequence 324 AA;
 Query Match 18.0%; Score 57; DB 5; Length 324;
 Best Local Similarity 100.0%; Pred. No. 9.5e-44;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EARLHMPMYLLQLSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 108
 DB 60 EARLHMPMYLLQLSLMDLLFTSVTPKALADFLRRENTISFGGCAIQMFALTMG 116

RESULT 14
 AAG73027
 ID AAG73027 standard; protein; 234 AA.

AC AAG73027;

DT 30-JUL-2001 (first entry)

DE Olfactory receptor-like polypeptide, SEQ ID NO: 2709.

XX Human; olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation.
 XX

OS Unidentified.

PN WO200127158-A2.

PD 19-APR-2001.

PR 06-OCT-2000; 2000WO-US027582.

PR 08-OCT-1999; 99US-0158615P.

PR 24-FEB-2000; 2000US-0184809P.
 XX (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I;
 XX WPI, 2001-290713/30.
 DR
 XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 PT
 PS Example 6; Page 1832-1833; 1857pp; English.
 CC The present sequence is an olfactory receptor polypeptide which was used
 CC as a query sequence in a database search of olfactory receptor (OR)-like
 CC sequences. The invention relates to isolated polynucleotides encoding
 CC polypeptides involved in olfactory sensation. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification of
 CC the odour receptors used to detect these primary scents. The methods also
 CC enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC facilities of different individuals
 CC
 XX
 SQ Sequence 234 AA;
 Query Match 4.7%; Score 15; DB 4; Length 234;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVALCHPLKY 132
 DB 60 MAYDRYVALCHPLKY 74

RESULT 15
 AAB71196
 ID AAB71196 standard; protein; 316 AA.

AC AAB71196;

DT 12-NOV-2002 (first entry)

DE Human GPCR protein SEQ ID 68.

XX Human; anti-HIV; nootropic; antiasthmatic; antiarteriosclerotic; GPCR;
 KW immunosuppressive; immunomodulator; cyostatic; antiinflammatory; AIDS;
 KW antidiabetic; neuroprotective; anorectic; haemostatic; antibacterial;
 KW fungicide; protozoal; vitinicide; human G-protein coupled receptor;
 KW gene therapy; vaccine; cardiomyopathy; atherosclerosis; diabetes;
 KW cell signal processing; cancer; obesity; neurodegenerative disorder;
 KW cachexia; anorexia; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; graft versus host disease; bronchial asthma;
 KW Crohn's disease; multiple sclerosis; haemophilia; infectious disease;
 KW idiopathic thrombocytopenic purpura; receptor.

OS Homo sapiens.

PN WO200250275-A2.

PD 27-JUN-2002.

PR 18-DEC-2001; 2001WO-US048958.

PR 18-DEC-2000; 2000US-0256635P.

PR 21-DEC-2000; 2000US-0257876P.

PR 04-JAN-2001; 2001US-0259743P.

PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX

(CURA-) CURAGEN CORP.

PI Padigaru M, Kekuda R, Li L, Ballinger RA, Casman SU, Spytek KA;
PI Baumgartner JC, Burgess CE;
XX

DR WPI; 2002-657419/70.
DR N-PSDB; AAF88435.
XX

PT New G-protein coupled receptor polypeptides, useful in gene therapy,
PT particularly for treating or preventing cardiomyopathy, atherosclerosis,
PT diabetes, Crohn's disease, hemophilia or cancer in humans.
XX

PS Claim 1; Page 112; 155pp; English.

XX
CC This invention describes novel human G-protein coupled receptor (GPCRX)
CC polypeptides which have anti-HIV, nootropic, antiasthmatic, protozoal,
CC antiarteriosclerotic, immunosuppressive, immunomodulator, cytostatic,
CC antiinflammatory, antidiabetic, neuroprotective, anorectic, haemostatic,
CC antibacterial, fungicide and virucide activity. The products of the
CC invention can be used in gene therapy or for vaccines. The GPCRX
CC polypeptide, GPCRX nucleic acid and antibody are useful for treating,
CC preventing or alleviating a GPCRX-associated disorder or a pathological
CC state in a subject e.g. cardiomyopathy, atherosclerosis, diabetes, or a
CC disorder related to cell signal processing and metabolic pathway
CC modulation. The GPCRX polypeptide and nucleic acid are also useful for
CC diagnosing the presence of or predisposition to a disease associated with
CC altered levels of GPCRX, particularly cancer. These polypeptides, nucleic
CC acids and antibodies are also useful for treating or preventing obesity,
CC Alzheimer's disease, Parkinson's disease, cancer-associated cachexia, anorexia,
CC host disease, bronchial asthma, Crohn's disease, immune disorders, graft versus
CC haemophilia, idiopathic thrombocytopenic purpura or infectious disease.
CC They can also be used to screen for potential agonist and antagonist
CC compounds. The polypeptides are also useful as immunogens to produce
CC antibodies or as vaccines. Anti-GPCRX antibodies can be used
CC diagnostically to monitor protein levels in tissue as part of a clinical
CC testing procedure such as in determining the efficacy of a given
CC treatment regimen. The host cells are useful in producing non-human
CC transgenic animals which are useful for studying the function and/or
CC activity of GPCRX protein and for identifying and/or evaluating
CC modulators of GPCRX protein activity. AAB71163-AAB71226 represent the
CC human GPCRX proteins encoded by AAF88402-AAF88465
XX

SQ Sequence 316 AA;

Query Match 4.7%; Score 15; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHPUKY 132
DB 124 MAYDRYVAICHPUKY 138

Search completed: October 5, 2004, 14:21:37
Job time : 127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 14:18:09 ; Search time 40 Seconds

(without alignments)
759.913 Million cell updates/sec

Title: US-10-024-444b-2

Perfect score: 316

Sequence: 1 MELNSTLGGSGFIIVGLND.....VWRALRYLTKYILLASHSL 316

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR 78:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	4.7	234	2	S28999
2	13	4.1	232	2	S29001
3	13	4.1	311	2	JCS200
4	13	4.1	315	2	JCS201
5	13	4.1	327	2	F23701
6	12	3.8	333	2	A23701
7	11	3.5	222	2	D40745
8	11	3.5	304	2	S29709
9	11	3.5	309	1	S51356
10	11	3.2	165	2	S28997
11	10	3.2	168	2	S28997
12	10	3.2	215	2	S28997
13	10	3.2	216	2	S28997
14	10	3.2	216	2	S28997
15	10	3.2	222	2	S28997
16	10	3.2	222	2	S28997
17	10	3.2	222	2	S28997
18	10	3.2	225	2	S28997
19	10	3.2	307	2	S28997
20	10	3.2	310	2	S28997
21	10	3.2	312	2	S28997
22	10	3.2	312	2	S28997
23	10	3.2	312	2	S28997
24	10	3.2	312	2	S28997
25	10	3.2	312	2	S28997
26	10	3.2	312	2	S28997
27	10	3.2	312	2	S28997
28	10	3.2	312	2	S28997
29	10	3.2	312	2	S28997

30	9	2.8	157	2	S58073	probable olfactory
31	9	2.8	315	2	JCS836	olfactory receptor
32	9	2.8	367	2	J49022	kappa opioid recep
33	9	2.8	367	2	JCS2421	opioid receptor ho
34	9	2.8	367	2	S43087	G protein-coupled
35	9	2.8	370	2	S43087	orphan opioid rece
36	9	2.8	370	2	AG3073	hypothetical prote
37	9	2.8	370	2	AG3073	probable maltose/m
38	9	2.5	147	2	B98213	hypothetical prote
39	8	2.5	157	2	S58000	probable olfactory
40	8	2.5	157	2	S58029	probable olfactory
41	8	2.5	157	2	S58037	probable olfactory
42	8	2.5	168	2	G95023	probable olfactory
43	8	2.5	168	2	H97894	acetyltransferase,
44	8	2.5	171	2	B71147	hypothetical prote
45	8	2.5	180	2	B97200	probable phosphata

ALIGNMENTS

RESULT 1

S28999

G:Protein-coupled receptor (clone PTE38) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998

C/Accession: S28999

R:Abe, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S.

FEBS Lett. 316, 253-256, 1993

A>Title: Multiple genes for G protein-coupled receptors and their expression in lingual

A/Reference number: S28996; PMID:9318133; PMID:8380780

A/Accession: S28999

A:Molecule type: mRNA

A:Residues: 1234 <AB>

C:Superfamily: Olfactory receptor OR14

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 4.7%; Score 15; DB 2; Length 234;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 60 MAYDRYVAICHPDKY 74

RESULT 2

S29001

G:Protein-coupled receptor (clone PTE58) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998

C/Accession: S29001

R:Abe, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S.

FEBS Lett. 316, 253-256, 1993

A>Title: Multiple genes for G protein-coupled receptors and their expression in lingual

A/Reference number: S28996; PMID:9318133; PMID:8380780

A/Accession: S29001

A:Molecule type: mRNA

A:Residues: 1-232 <AB>

C:Superfamily: olfactory receptor OR14

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 4.1%; Score 13; DB 2; Length 232;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 58 MAYDRYVAICHPDKY 70

RESULT 3

JCS200

Chemoreceptor TB334 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
 C/Accession: JCS200; PC4302
 R/Thomas, M.B.; Haines, S.L.; Akesson, R.A.
 Gene 178, 1-5, 1996
 A/Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
 A/Reference number: JCS200; MUID:97080538; PMID:8921883
 A/Accession: JCS200
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-311 <THO1>
 A/Cross-references: GB:U50947; NID:g1256388; PIDN:AACS2909.1; PID:g1256389
 A/Accession: PC4302
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 146-153;265-272 <THO2>
 A/Experimental source: taste bud
 C/Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
 C/Genetics:
 A/Gene: tb334
 C/Superfamily: olfactory receptor OR14
 C/Keywords: olfaction; taste bud; transmembrane protein
 F/24-47/Domain: transmembrane #status predicted <TM1>
 F/56-77/Domain: transmembrane #status predicted <TM2>
 F/99-118/Domain: transmembrane #status predicted <TM3>
 F/138-162/Domain: transmembrane #status predicted <TM4>
 F/195-217/Domain: transmembrane #status predicted <TM5>
 F/236-258/Domain: transmembrane #status predicted <TM6>
 F/271-291/Domain: transmembrane #status predicted <TM7>

Query Match 4.1%; Score 13; DB 2; Length 311;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHP 130
 |||||
 DB 116 MAYDRYVAICHP 128

RESULT 4
 JCS201
 Chemoreceptor TB567 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
 C/Accession: JCS201; PC4303
 R/Thomas, M.B.; Haines, S.L.; Akesson, R.A.
 Gene 178, 1-5, 1996
 A/Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
 A/Reference number: JCS200; MUID:97080538; PMID:8921883
 A/Accession: JCS201
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-315 <THO1>
 A/Cross-references: GB:U50948; NID:g1256390; PIDN:AACS2910.1; PID:g1256391
 A/Accession: PC4303
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 144-151;270-277 <THO2>
 A/Experimental source: taste bud
 C/Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
 C/Genetics:
 A/Gene: tb567
 C/Superfamily: olfactory receptor OR14
 C/Keywords: olfaction; taste bud; transmembrane protein
 F/26-49/Domain: transmembrane #status predicted <TM1>
 F/58-79/Domain: transmembrane #status predicted <TM2>
 F/101-120/Domain: transmembrane #status predicted <TM3>
 F/140-164/Domain: transmembrane #status predicted <TM4>
 F/197-219/Domain: transmembrane #status predicted <TM5>
 F/238-260/Domain: transmembrane #status predicted <TM6>
 F/273-293/Domain: transmembrane #status predicted <TM7>

Query Match 4.1%; Score 13; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 INPLIYSLRNKEV 297
 |||||
 DB 285 INPLIYSLRNKEV 297

RESULT 5
 F23701
 Olfactory receptor I7 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C/Accession: F23701
 R/Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A/Reference number: A23701; MUID:91191556; PMID:1840504
 A/Accession: F23701
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-327 <BUC>
 A/Cross-references: GB:M64386; NID:g205833; PIDN:AAA41749.1; PID:g205834
 C/Superfamily: olfactory receptor OR14
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.1%; Score 13; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHP 130
 |||||
 DB 123 MAYDRYVAICHP 135

RESULT 6
 A23701
 Olfactory receptor F3 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C/Accession: A23701
 R/Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A/Reference number: A23701; MUID:91191556; PMID:1840504
 A/Accession: A23701
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-333 <BUC>
 A/Cross-references: GB:M64376; NID:g205813; PIDN:AAA41739.1; PID:g205814
 C/Superfamily: olfactory receptor OR14
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.8%; Score 12; DB 2; Length 333;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHP 129
 |||||
 DB 118 MAYDRYVAICHP 129

RESULT 7
 D40745
 Odorant receptor (clone K4) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 03-Nov-2000
 C/Accession: D40745
 R/Reisler, K.U.; Sullivan, S.L.; Buck, L.B.
 Cell 73, 597-609, 1993
 A/Title: A zonal organization of odorant receptor gene expression in the olfactory epith
 A/Reference number: A40745; MUID:93258822; PMID:7683976

A/Accession: D40745
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-222 <RES>
A/Cross-references: GB:114566; NID:9293753; PIDN:AAA39850.1; PID:g293754
A/Experimental source: olfactory epithelium
A/Note: sequence extracted from NCBI backbone (NCBIP:131753)
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match
Best Local Similarity 3.5%; Score 11; DB 2; Length 222;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 YDRYVAICHP 130
DB 60 YDRYVAICHP 70

RESULT 8

S29709
Olfactory receptor OR14 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
R/Ramung, K.; Krieger, J.; Strommann, J.; Boekhoff, I.; Knidick, S.; Baumstark, C.; Breez
Nature 361, 353-356, 1993
A/Title: Cloning and expression of odorant receptors.
A/Reference number: S29707; MUID:93149273; PMID:7678922
A/Accession: S29709
A/Molecule type: mRNA
A/Residues: 1-304 <RAM>
C/Superfamily: olfactory receptor OR14

Query Match
Best Local Similarity 3.5%; Score 11; DB 2; Length 304;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 LNPLYSLRNK 295
DB 278 LNPLYSLRNK 288

RESULT 9

S51356
Olfactory receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S51356; S47014
R/Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
Eur. J. Biochem. 225, 1157-1168, 1994
A/Title: Olfactory receptor proteins: Expression, characterization and partial purification
A/Reference number: S51356; MUID:95045546; PMID:7957207
A/Accession: S51356
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-309 <GAT>
R/Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
submitted to the EMBL Data Library, July 1994
A/Description: Olfactory receptor proteins: expression, characterization and partial pur
A/Reference number: S47014
A/Accession: S47014
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-309 <GAT>
A/Cross-references: EMBL:X80671; NID:9517365; PIDN:CA56697.1; PID:9517366
C/Superfamily: olfactory receptor OR14

Query Match
Best Local Similarity 3.5%; Score 11; DB 1; Length 309;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 LNPLYSLRNK 295
DB 286 LNPLYSLRNK 296

RESULT 10

138471
Olfactory receptor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C/Accession: 138471
R/Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozz
Hum. Mol. Genet. 3, 229-235, 1994
A/Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication c
A/Reference number: 138470; MUID:94272458; PMID:8004088
A/Accession: 138471
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-165 <RES>
A/Cross-references: EMBL:U04678; NID:9438390; PIDN:AAA18343.1; PID:g438391
A/Gene: OR17-4
C/Superfamily: olfactory receptor OR14

Query Match
Best Local Similarity 3.2%; Score 10; DB 2; Length 165;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAIC 127
DB 1 MAYDRYVAIC 10

RESULT 11

S28997
G protein-coupled receptor (clone PTE03) - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C/Accession: S28997
R/Abc, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S.
FEBS Lett. 316, 253-256, 1993
A/Title: Multiple genes for G protein-coupled receptors and their expression in lingual
A/Reference number: S28996; MUID:93138133; PMID:8380780
A/Accession: S28997
A/Molecule type: mRNA
A/Residues: 1-168 <ABE>
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match
Best Local Similarity 3.2%; Score 10; DB 2; Length 168;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAIC 127
DB 43 MAYDRYVAIC 52

RESULT 12

138473
Olfactory receptor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C/Accession: 138473
R/Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozz
Hum. Mol. Genet. 3, 229-235, 1994
A/Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication of
A/Reference number: 138470; MUID:94272458; PMID:8004088
A/Accession: 138473
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-215 <RES>
A/Cross-references: EMBL:U04681; NID:9438395; PIDN:AAA18345.1; PID:g438396

C:Genetics:
A:Gene: OR17-30
C:Superfamily: olfactory receptor OR14

Query Match 3.2%; Score 10; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 MAYDRYVAIC 127
DB 51 MAYDRYVAIC 60

RESULT 13

138470
Olfactory receptor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C:Accession: I38470
R:Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozzo, Hum. Mol. Genet. 3, 229-235, 1994
A:Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication of
A:Reference number: I38470; MUID:94272458; PMID:8004088
A:Accession: I38470
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-216 <RES>
A:Cross-references: EMBL:U04642; NID:G438388; PIDN:AAA17447.1; PID:G438389
C:Genetics:
A:Gene: OR17-2
C:Superfamily: olfactory receptor OR14

Query Match 3.2%; Score 10; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 MAYDRYVAIC 127
DB 51 MAYDRYVAIC 60

RESULT 14

138474
Olfactory receptor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C:Accession: I38474
R:Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozzo, Hum. Mol. Genet. 3, 229-235, 1994
A:Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication of
A:Reference number: I38470; MUID:94272458; PMID:8004088
A:Accession: I38474
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-216 <RES>
A:Cross-references: EMBL:U04682; NID:G438397; PIDN:AAA18346.1; PID:G438398
C:Genetics:
A:Gene: OR17-32
C:Superfamily: olfactory receptor OR14

Query Match 3.2%; Score 10; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 MAYDRYVAIC 127
DB 51 MAYDRYVAIC 60

RESULT 15

C40745
Olfactory receptor (clone K7) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C:Accession: C40745
R:Resler, K.J.; Sullivan, S.L.; Buck, L.B.
Cell 73, 597-609, 1993

A:Title: A zonal organization of odorant receptor gene expression in the olfactory epithelium
A:Reference number: A40745; MUID:93258822; PMID:7683976
A:Accession: C40745
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-222 <RES>

A:Cross-references: GB:L14569; NID:G293759; PIDN:AAA39853.1; PID:G293760
A:Experimental source: olfactory epithelium
A>Note: sequence extracted from NCBI backbone (NCBIP.131750)
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 10; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 MAYDRYVAIC 127
DB 58 MAYDRYVAIC 67

Search completed: October 5, 2004, 14:24:54
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 14:09:18 ; Search time 25 Seconds

(without alignments)
658.167 Million cell updates/sec

Title: US-10-024-444B-2
Perfect score: 316
Sequence: 1 MELNSTLGGSGFLIVGLIND.....VMRALRVLYGKYLIIAHLSTL 316

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size: 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	18.0	316	02AG_HUMAN	G9h205 homo sapien
2	15	4.7	234	1 GUS8_RAT	P35897 rattus norv
3	14	4.4	317	1 OAD1_HUMAN	O8ng60 homo sapien
4	13	4.1	216	1 O1N1_HUMAN	O43870 homo sapien
5	13	4.1	216	1 O2M4_HUMAN	O96127 homo sapien
6	13	4.1	232	1 GUS8_RAT	P35899 rattus norv
7	13	4.1	280	1 O1J5_HUMAN	O9n2p1 homo sapien
8	13	4.1	309	1 O5AK_HUMAN	O8n1b0 homo sapien
9	13	4.1	309	1 O5AK_HUMAN	O8n3g7 homo sapien
10	13	4.1	310	1 O9Q1_HUMAN	O8ng97 homo sapien
11	13	4.1	311	1 O1N3_HUMAN	O8ng95 homo sapien
12	13	4.1	311	1 O8H1_HUMAN	O8ng94 homo sapien
13	13	4.1	312	1 O2M6_HUMAN	O8ng81 homo sapien
14	13	4.1	312	1 O2M7_HUMAN	O8ng82 homo sapien
15	13	4.1	312	1 O8H2_HUMAN	O8ng83 homo sapien
16	13	4.1	312	1 O8H2_HUMAN	O8ng81 homo sapien
17	13	4.1	313	1 O8H2_HUMAN	O8ng81 homo sapien
18	13	4.1	313	1 O1J2_HUMAN	O8ng95 mus musculu
19	13	4.1	313	1 O1J4_HUMAN	O8ng92 homo sapien
20	13	4.1	314	1 O2A4_HUMAN	O8ng81 homo sapien
21	13	4.1	314	1 O1C1_HUMAN	O15619 homo sapien
22	13	4.1	314	1 O8H2_HUMAN	O8ng81 mus musculu
23	13	4.1	314	1 O8H2_HUMAN	O8ng81 mus musculu
24	13	4.1	314	1 O8H2_HUMAN	O8ng81 mus musculu
25	13	4.1	314	1 O8H2_HUMAN	O8ng81 mus musculu
26	13	4.1	315	1 O2A6_HUMAN	O8ng85 homo sapien
27	13	4.1	317	1 O6O1_HUMAN	O8n1b5 homo sapien
28	13	4.1	319	1 O8K1_HUMAN	O8ng92 homo sapien
29	13	4.1	319	1 O8K1_HUMAN	O8ng92 homo sapien
30	13	4.1	319	1 O8K1_HUMAN	O8ng92 homo sapien
31	13	4.1	320	1 O2T4_HUMAN	O8ng81 mus musculu
32	13	4.1	320	1 O5C1_HUMAN	O8n1b0 homo sapien
33	13	4.1	322	1 O1J1_HUMAN	O8ng83 homo sapien

ALIGNMENTS

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34 13 4.1 324 1 O7G2_HUMAN      O8ng99 homo sapien
35 13 4.1 327 1 O1F7_RAT       P23270 rattus norv
36 13 4.1 331 1 O5E3_HUMAN      O8ngw1 homo sapien
37 13 4.1 333 1 O7G1_HUMAN      O8ng90 homo sapien
38 13 4.1 337 1 O1FC_HUMAN      O8nha8 homo sapien
39 12 3.8 309 1 O5K3_HUMAN      O8nha9 homo sapien
40 12 3.8 311 1 O5AN_HUMAN      O8ngi7 homo sapien
41 12 3.8 311 1 O5AN_HUMAN      O8ng18 homo sapien
42 12 3.8 311 1 O5P3_HUMAN      O8w294 homo sapien
43 12 3.8 314 1 O8K2_MOUSE      O8ngj0 mus musculu
44 12 3.8 315 1 O5A1_HUMAN      O8ngj0 mus musculu
45 12 3.8 322 1 O5P2_HUMAN      O8w292 homo sapien

RESULT 1
ID O2AG_HUMAN          STANDARD;          PRT;          316 AA.
AC O9H205; O96R26;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 2AG1 (HTJ).
GN OR2AG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RL receptor genes."
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 68-284 FROM N.A.
RX MEDLINE=22202146; PubMed=12213199;
RA Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA Leirich H., Lancel D., Shamir R.;
RT "DEFOG: a practical scheme for deciphering families of genes."
RN [3]
RP SEQUENCE OF 152-316 FROM N.A.
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RL loci."
RN [4]
RP Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDEx);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDEx/showgene.pl?key=symbol&
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB065823; BAC06042.1; -
DR EMBL; AF399618; AAK95103.1; -
DR EMBL; AF321237; AAG45209.1; -
DR Genew; HGNC:15142; OR2AG1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

```

PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSMEM 26 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 120
 FT DOMAIN 121 139
 FT TRANSMEM 140 158
 FT DOMAIN 159 195
 FT TRANSMEM 196 219
 FT DOMAIN 220 236
 FT TRANSMEM 237 259
 FT DOMAIN 260 272
 FT TRANSMEM 273 292
 FT DOMAIN 293 316
 FT DISULFID 97 189
 FT CARBOHYD 5 5
 FT CARBOHYD 19 19
 FT CONFLICT 187 187
 FT CONFLICT 299 299
 SQ SEQUENCE 316 AA; 35270 MW; 6885161BD06C0AE CRC64;
 Query Match 18.0%; Score 57; DB 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1,1e-48;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

52 EARLHMPYLLIGQLSLMDLFTSVTPKALADLRRENTISFGGCAIQMFLATIMG 108
 52 EARLHMPYLLIGQLSLMDLFTSVTPKALADLRRENTISFGGCAIQMFLATIMG 108

RESULT 2
 GU38_RAT STANDARD; PRT; 234 AA.
 ID GU38_RAT
 AC P35897;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Possible gustatory receptor clone PTB38 (Fragment).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer; TISSUE=Lingual epithelium;
 RX MEDLINE=9318133; PubMed=8380780;
 RA Abe K., Kusakabe Y., Tanemura K., Emori Y., Arai S.;
 RT "Multiple genes for G-protein-coupled receptors and their expression
 in lingual epithelia.";
 RL FEBS Lett. 316:253-256(1993).
 CC -1- FUNCTION: Possible taste receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Tongue specific.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT NON TER 1 1
 FT TRANSMEM <1 11
 FT DOMAIN 12 42
 FT TRANSMEM 43 62
 FT DOMAIN 63 84
 FT TRANSMEM 85 105
 FT DOMAIN 106 138
 FT TRANSMEM 139 160
 5 (POTENTIAL).
 2 (POTENTIAL).
 3 (POTENTIAL).
 4 (POTENTIAL).
 5 (POTENTIAL).

FT DOMAIN 161 182
 FT TRANSMEM 183 202
 FT DOMAIN 203 212
 FT TRANSMEM 213 234
 FT DISULFID 39 121
 FT NON TER 234 234
 SQ SEQUENCE 234 AA; 26375 MW; B4506DD948080003 CRC64;
 Query Match 4.7%; Score 15; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 4.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

118 MAYDRYVAICHPKXY 132
 60 MAYDRYVAICHPKXY 74

RESULT 3
 OADI_HUMAN STANDARD; PRT; 317 AA.
 ID OADI_HUMAN
 AC O8NGEO;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 10ADI.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsuni S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
 WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&

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 or send an email to license@sib-sib.ch).
 CC EMBL; AB065872; BAC06090.1; -
 CC Genew; HGNC:14819; OR10AD1.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSMEM 26 46
 FT DOMAIN 47 55
 FT TRANSMEM 56 76
 FT DOMAIN 77 100
 FT TRANSMEM 101 121
 FT DOMAIN 122 140
 FT TRANSMEM 141 161
 FT DOMAIN 162 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 238
 FT TRANSMEM 239 259
 FT DOMAIN 260 272
 1 (POTENTIAL).
 2 (POTENTIAL).
 3 (POTENTIAL).
 4 (POTENTIAL).
 5 (POTENTIAL).
 6 (POTENTIAL).
 7 (POTENTIAL).
 6 (POTENTIAL).
 7 (POTENTIAL).

FT TRANSMEM 273 293 7 (POTENTIAL).
 FT DOMAIN 294 317 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 98 190 BY SIMILARITY.
 FT CAROHXD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 317 AA; 35698 MW; 72D856594467060F CRC64;

Query Match 4.4%; Score 14; DB 1; Length 317;
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LIAFMAYDRYVAIC 127
 DB 115 LIAFMAYDRYVAIC 128

RESULT 4

01N1 HUMAN STANDARD; PRT; 216 AA.

AC 043870;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 1N1 (Olfactory receptor 1-26) (OR1-26) (Fragment).
 GN OR1N1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98160182; PubMed=9500546;
 RA Rouquier S., Taviaux S., Traak B.J., Brand-Arpon V., van den Engh G.,
 RT Demaille J.G., Giorgi D.;
 RL "Distribution of olfactory receptor genes in the human genome."; Nat. Genet. 18:243-250(1998).
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
 WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbols

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 CC -----
 CC EMBL; U86216; AAC39612.1; -
 CC Genew; HGNC:8221; OR1N1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 Olfaction.
 FT NON TER 1 1
 FT TRANSMEM 1 1
 FT DOMAIN <1 12 2 (POTENTIAL).
 FT TRANSMEM 13 33 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 34 53 3 (POTENTIAL).
 FT TRANSMEM 54 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 91 4 (POTENTIAL).
 FT TRANSMEM 92 129 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 130 152 5 (POTENTIAL).
 FT TRANSMEM 153 169 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 170 192 6 (POTENTIAL).
 FT DOMAIN 193 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 >216 7 (POTENTIAL).
 FT DISULFID 30 122 BY SIMILARITY.
 FT NON TER 216 216

SQ SEQUENCE 216 AA; 23896 MW; E27DA3AE1E2C50BE CRC64;

Query Match 4.1%; Score 13; DB 1; Length 216;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHP 130
 DB 51 MAYDRYVAICHP 130

RESULT 5

02M4 HUMAN STANDARD; PRT; 216 AA.

AC 096827; Q15611;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 2M4 (Olfactory receptor TPCN100) (OST710)
 DE (HTPCRX18) (Fragment).
 GN OR2M4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22202146; PubMed=12213199;
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
 RA Shmulevich D., Elkon R., Steinfach M., O'Brien J.K., Radolof U.,
 RA Lehnach H., Lancet D., Shamir R.;
 RT "DEPOG: a practical scheme for deciphering families of genes."; Genomics 80:295-302(2002).
 RL [2]
 RP SEQUENCE OF 59-215 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97224452; PubMed=9119360;
 RA Vanderaeghe P., Schurmann S., Vassart G., Parmentier M.;
 RT "Specific repertoire of olfactory receptor genes in the male germ
 RT cells of several mammalian species."; Genomics 39:239-246(1997).
 RL [3]
 RP SEQUENCE OF 59-172 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=9211132; PubMed=1370859;
 RA Parmentier M., Libert F., Schurmann S., Schiffmann S., Lefort A.,
 RA Eggerickx D., Ledent C., Mollereau C., Gerard C., Perret J.,
 RA Goerkegeon A., Vassart G.;
 RT "Expression of members of the putative olfactory receptor gene family
 RT in mammalian germ cells."; Nature 355:453-455(1992).
 RL Nature 355:453-455(1992).
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
 WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbols

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 CC -----
 CC EMBL; AF399617; AAK95102.1; -
 CC EMBL; X89666; CA61813.1; -
 CC EMBL; X64992; -; NOT_ANNOTATED_CDS.
 DR PIR; S58011; S58011.
 DR Genew; HGNC:8270; OR2M4.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodpsn.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Multigene family;
 KM Olfaction.
 FT NON TER 1 12 2 (POTENTIAL).
 FT TRANSMEM <1 13 33 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 13 33 3 (POTENTIAL).
 FT TRANSMEM 54 53 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 72 72 4 (POTENTIAL).
 FT TRANSMEM 73 91 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 92 128 5 (POTENTIAL).
 FT TRANSMEM 129 152 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 153 169 6 (POTENTIAL).
 FT TRANSMEM 170 192 6 (POTENTIAL).
 FT DOMAIN 193 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 >216 7 (POTENTIAL).
 FT DISULFID 30 122 BY SIMILARITY.
 FT CONFLICT 214 215 LT -> SH (IN REF. 2).
 FT NON TER 216 216
 SQ SEQUENCE 216 AA; 23872 MW; DE7432325A5ACF9 CRC64;
 Query Match 4.1%; Score 13; DB 1; Length 216;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 118 MAYDRYVALCHPL 130
 DB 51 MAYDRYVALCHPL 63
 RESULT 6
 GUS8_RAT STANDARD; PRT; 232 AA.
 AC P35899;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Possible gustatory receptor clone PR58 (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fi3ch3; TISSUE=Lingual epithelium;
 RX MEDLINE=93138133; PubMed=8380780;
 RA Abe K., Kusakabe Y., Tanemura K., Emori Y., Arai S.;
 RT "Multiple genes for G protein-coupled receptors and their expression
 in lingual epithelia."
 RL FEBS Lett. 316:253-256(1993).
 CC -1- FUNCTION: Possible taste receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Tongue specific.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT NON TER 1 1 2 (POTENTIAL).
 FT TRANSMEM <1 9 3 (POTENTIAL).
 FT DOMAIN 10 40 4 (POTENTIAL).
 FT TRANSMEM 41 60 3 (POTENTIAL).
 FT DOMAIN 61 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 4 (POTENTIAL).
 FT DOMAIN 104 136 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 137 158 5 (POTENTIAL).
 FT DOMAIN 159 180 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 181 200 6 (POTENTIAL).
 FT DOMAIN 201 210 6 (POTENTIAL).
 FT TRANSMEM 211 232 7 (POTENTIAL).
 FT DISULFID 37 119 BY SIMILARITY.
 FT NON TER 232 232
 SQ SEQUENCE 232 AA; 25695 MW; 2B72EAB08A992B7 CRC64;

Query Match 4.1%; Score 13; DB 1; Length 232;
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 118 MAYDRYVALCHPL 130
 DB 58 MAYDRYVALCHPL 70
 RESULT 7
 ID OJ5_HUMAN STANDARD; PRT; 280 AA.
 AC OGNZPL;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 1J5 (HSAS) (HTPCX15) (Fragment).
 GN OR1J5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 91-252 FROM N.A.
 RX MEDLINE=20183981; PubMed=10706615;
 RA Rouquier S., Blancher A., Giorgi D.,
 RT "The olfactory receptor gene repertoire in primates and mouse:
 Evidence for reduction of the functional fraction in primates."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
 RN [2]
 RP SEQUENCE OF 93-206 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=92131132; PubMed=1370859;
 RA Parmentier M., Libert F., Schumann S., Schiffmann S., Lefort A.,
 RA Eggerickx D., Legend C., Mollereau C., Gerard C., Pernet J.,
 RA Eggerickx A., Vassart G.,
 RT "Expression of members of the putative olfactory receptor gene family
 in mammalian germ cells."
 RL Nature 355:453-455(1992).
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAMB=Human Olfactory Receptor Data Explorer (HORDE);
 WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&

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 or send an email to license@sib-sib.ch).

 CC EMBL: AF179767; AAF40352.1; -;
 DR EMBL: X64989; -; NOT ANNOTATED_CDS.
 DR Genew: HGNC:15109; OR1J5.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KM Olfaction.
 FT NON TER 1 1 1 (POTENTIAL).
 FT TRANSMEM <1 16 1 (POTENTIAL).
 FT DOMAIN 17 24 2 (POTENTIAL).
 FT TRANSMEM 25 46 3 (POTENTIAL).
 FT DOMAIN 47 67 3 (POTENTIAL).
 FT TRANSMEM 68 87 3 (POTENTIAL).
 FT DOMAIN 88 106 4 (POTENTIAL).
 FT TRANSMEM 107 125 4 (POTENTIAL).
 FT DOMAIN 126 163 5 (POTENTIAL).
 FT TRANSMEM 164 186

FT DOMAIN 187 203 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 204 226 6 (POTENTIAL).
 FT DOMAIN 227 239 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 240 259 7 (POTENTIAL).
 FT DOMAIN 260 280 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 64 156 BY SIMILARITY.
 FT CONFLICT 115 115 S -> T (IN REF. 1).
 SQ SEQUENCE 280 AA; 31788 MW; 3ACC2B01C948791D CRC64;

Query Match 4.1%; Score 13; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 118 MAYDRYVAICHL 130
 Db 85 MAYDRYVAICHL 97

RESULT 8
 ID OSAK HUMAN STANDARD; PRT; 309 AA.
 AC O8NH90;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 5AK2.
 GN OR5AK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Teutsuni S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&

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DR EMBL; AB065496; BAC05747.1; -;
 DR Genew; HGNC:15251; OR5AK2.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; FALSE_NEG.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 CC
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 46 1 (POTENTIAL).
 FT DOMAIN 47 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 75 2 (POTENTIAL).
 FT DOMAIN 76 99 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 100 120 3 (POTENTIAL).
 FT DOMAIN 121 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 154 4 (POTENTIAL).
 FT DOMAIN 155 196 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 197 217 5 (POTENTIAL).
 FT DOMAIN 218 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 258 6 (POTENTIAL).
 FT DOMAIN 259 271 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 272 292 7 (POTENTIAL).
 FT DOMAIN 293 309 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 309 AA; 34627 MW; 6022418115A44AC4 CRC64;

Query Match 4.1%; Score 13; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 285 LNPILYSLRNKEV 297
 Db 285 LNPILYSLRNKEV 297

RESULT 9
 ID O8A1 HUMAN STANDARD; PRT; 309 AA.
 AC O8NG67; O96RC6;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 8A1 (OST025).
 GN OR8A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Teutsuni S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&

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DR EMBL; AB065833; BAC06052.1; -;
 DR EMBL; AF399512; AAK94997.1; -;
 DR Genew; HGNC:8469; OR8A1.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 CC
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 46 1 (POTENTIAL).
 FT DOMAIN 47 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 75 2 (POTENTIAL).

FT DOMAIN 76 99 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 100 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 160 4 (POTENTIAL).
 FT DOMAIN 161 196 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 197 216 5 (POTENTIAL).
 FT DOMAIN 217 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 257 6 (POTENTIAL).
 FT DOMAIN 258 270 7 (POTENTIAL).
 FT TRANSMEM 271 291 7 (POTENTIAL).
 FT DOMAIN 292 309 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 188 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 309 AA; 34395 MW; 202DEB98B0F4BEEB CRC64;
 Query Match 4.1%; Score 13; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 118 MAYDRYVAICHEL 130
 DB 118 MAYDRYVAICHEL 130
 RESULT 10
 09Q1 HUMAN STANDARD; PRT; 310 AA.
 AC Q8NGQ5; Q96RA7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 9Q1.
 GN OR9Q1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Teusuni S., Aburatani H., Asai K., Akiyama Y.,
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes."
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 66-282 FROM N.A.
 RA MEDLINE=2202146; PubMed=12213199;
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
 RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
 RA Lehnach H., Lancel D., Shamir R.,
 RT "DEFOG: a practical scheme for deciphering families of genes."
 RT Genomics 80:295-302(2002).
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. (HORD)
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORD);
 CC WWW="http://bioinformatics.weimann.ac.il/cgi-bin/HORD/showgene.pl?key=symbol&
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 CC EMBL: AB065734; BAC05955.1; -;
 CC EMBL: AR399532; AKG95017.1; -;
 CC Genew, HGNC:14724; OR9Q1.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.

DR PROSITE; PS50262; G PROTEIN RECP FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein;
 KM Multi-gene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 46 1 (POTENTIAL).
 FT DOMAIN 47 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 75 2 (POTENTIAL).
 FT DOMAIN 76 99 3 (POTENTIAL).
 FT TRANSMEM 100 120 3 (POTENTIAL).
 FT DOMAIN 121 139 4 (POTENTIAL).
 FT TRANSMEM 140 160 5 (POTENTIAL).
 FT DOMAIN 161 197 5 (POTENTIAL).
 FT TRANSMEM 198 217 6 (POTENTIAL).
 FT DOMAIN 218 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 257 7 (POTENTIAL).
 FT DOMAIN 258 270 7 (POTENTIAL).
 FT TRANSMEM 271 291 7 (POTENTIAL).
 FT DOMAIN 292 310 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 310 AA; 34756 MW; 6C27C347AB8BD741 CRC64;
 Query Match 4.1%; Score 13; DB 1; Length 310;
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 285 LNPILYSIRNKEV 297
 DB 284 LNPILYSIRNKEV 296
 RESULT 11
 01N3 HUMAN STANDARD; PRT; 311 AA.
 AC Q8NGQ5; Q96RA7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 1N3.
 GN OR1N3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Teusuni S., Aburatani H., Asai K., Akiyama Y.,
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes."
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 66-281 FROM N.A.
 RA MEDLINE=2202146; PubMed=12213199;
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
 RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
 RA Lehnach H., Lancel D., Shamir R.,
 RT "DEFOG: a practical scheme for deciphering families of genes."
 RT Genomics 80:295-302(2002).
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. (HORD)
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORD);
 CC WWW="http://bioinformatics.weimann.ac.il/cgi-bin/HORD/showgene.pl?key=symbol&
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DR EMBL: AB065719; BAC05940.1; -.
DR EMBL: AF399547; AAK95032.1; -.
DR Genew; HGNC:15112; ORIN3.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 23 EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM 24 47 1 (POTENTIAL) .
FT DOMAIN 48 55 CYTOPLASMIC (POTENTIAL) .
FT TRANSMEM 56 77 2 (POTENTIAL) .
FT DOMAIN 78 98 EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM 99 118 3 (POTENTIAL) .
FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL) .
FT TRANSMEM 138 156 4 (POTENTIAL) .
FT DOMAIN 157 194 EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM 195 217 5 (POTENTIAL) .
FT DOMAIN 218 234 CYTOPLASMIC (POTENTIAL) .
FT TRANSMEM 235 257 6 (POTENTIAL) .
FT DOMAIN 258 270 EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM 271 290 7 (POTENTIAL) .
FT DOMAIN 291 311 CYTOPLASMIC (POTENTIAL) .
FT DISULFID 95 187 BY SIMILARITY.
FT CARBOHYD 3 3 N-LINKED (GLCNAC... ) (POTENTIAL) .
SQ SEQUENCE 311 AA; 34650 MW; 6B82AEB0A4836180 CRC64;

Query Match
Best Local Similarity 4.1%; Score 13; DB 1; Length 311;
Matches 13; Conservativity 100.0%; Pred. No. 5.4e-05;
Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICBPL 130
|||||
116 MAYDRYVAICBPL 128

RESULT 12
08H1_HUMAN STANDARD; PRT; 311 AA.
ID ID_08H1_HUMAN
AC Q8NGG4;
DT 10-OCT-2003 (Rel. 42; Created)
DT 10-OCT-2003 (Rel. 42; Last sequence update)
DT 15-MAR-2004 (Rel. 43; Last annotation update)
DE Olfactory receptor BHL.
OS OR8H1.
GN Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsuni S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol";
CC -----
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CC -----
CC EMBL; AB065836; BAC06055.1; -.

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DR   Genew; HGNC:14824; ORH1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KM   Multigene family; Olfaction.
FT   DOMAIN                    1      25      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM                 26      46      1 (POTENTIAL).
FT   DOMAIN                   47      54      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM                55      75      2 (POTENTIAL).
FT   DOMAIN                  76      98      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM               99     119      3 (POTENTIAL).
FT   DOMAIN              120     138      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM            139     159      4 (POTENTIAL).
FT   DOMAIN             160     196      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM           197     216      5 (POTENTIAL).
FT   DOMAIN            217     236      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM          237     257      6 (POTENTIAL).
FT   DOMAIN            258     270      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM          271     291      7 (POTENTIAL).
FT   DOMAIN            292     311      CYTOPLASMIC (POTENTIAL).
FT   DISULFID              96     188      BY SIMILARITY.
FT   CARBOHYD              5       5      N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE    311 AA; 35227 MW; B2E548AEB0C2B2 CRC64;
Query Match                               4.1%; Score 13; DB 1; Length 311;
Best Local Similarity    100.0%; Pred. No. 5.4e-05;
Matches    13; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY      285 LNDPIYSLNKEV 297
        |||||
DB      284 LNDPIYSLNKEV 296

RESULT 13
O2M6_HUMAN STANDARD; PRT; 312 AA.
ID   O2M6_HUMAN
DC   Q8NGB3;
DT   15-MAR-2004 (Rel. 43, Created)
DI   15-MAR-2004 (Rel. 43, Last sequence update)
DE   15-MAR-2004 (Rel. 43, Last annotation update)
GN   Olfactory receptor 2M6.
OS   OR2M6.
SS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Explorerium (HORDE);
CC   WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&
-----
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entities requires a license agreement (See http://www.ebi.ac.uk/announcements
or send an email to license@ebi.ac.uk).
EMBL; AB065592; BAC06165.1; -.
Genew; HGNC:19593; OR2M6.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHDOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECIP_FL_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 45 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 196 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 259 6 (POTENTIAL).
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 311 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 312 AA; 34827 MW; 5CFE428A1948C2F2 CRC64;
 Query Match 4.1%; Score 13; DB 1; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 285 LNPLIYSIRNKEV 297
 Db 285 LNPLIYSIRNKEV 297
 RESULT 14
 ID 02M7 HUMAN STANDARD; PRT; 312 AA.
 AC Q8N681; 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 2M7.
 GN OR2M7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsun S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&
 CC www="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC EMBL; AB065954; BAC06167.1; -
 DR Genew; HGNC:19594; OR2M7.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHDOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECIP_FL_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 45 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 196 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 259 6 (POTENTIAL).
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 311 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 312 AA; 34902 MW; 42A9A1D7EB861E88 CRC64;
 Query Match 4.1%; Score 13; DB 1; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 285 LNPLIYSIRNKEV 297
 Db 285 LNPLIYSIRNKEV 297
 RESULT 15
 ID 08H2 HUMAN STANDARD; PRT; 312 AA.
 AC Q8N162; 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Olfactory receptor 8H2.
 GN OR8H2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsun S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&
 CC www="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AB065657; BAC05883.1; -
 DR Genew; HGNC:15308; OR8H2.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHDOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; FALSE_NEG.
 DR PROSITE; PS00262; G_PROTEIN_RECIP_FL_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multigene family; Olfaction.
 FT DOMAIN 1 26
 FT TRANSMEM 27 47
 FT DOMAIN 48 55
 FT TRANSMEM 56 76
 FT DOMAIN 77 99
 FT TRANSMEM 100 120
 FT DOMAIN 121 139
 FT TRANSMEM 140 160
 FT DOMAIN 161 197
 FT TRANSMEM 198 217
 FT DOMAIN 218 237
 FT TRANSMEM 238 258
 FT DOMAIN 259 271
 FT TRANSMEM 272 292
 FT DOMAIN 293 312
 FT DISULFID 97 189
 FT CARBOHYD 6
 SQ SEQUENCE 312 AA; 35422 MW; 0D5112EF980EC13E CRC64; N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 4.18; Score 13; DB 1; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 285 LNPLIYSLRNKEV 297
 |||||
 Db 285 LNPLIYSLRNKEV 297

Search completed: October 5, 2004, 14:22:10
 Job time : 31 secs

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OM protein - protein search, using sw model

Run on: October 5, 2004, 14:17:19 ; Search time 117 Seconds

(without alignments)
852.169 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1 MEINSTLGGSGFLVGLIND.....VMRALRVLYGKTYILLASTL 316

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP rvirus:*
16: SP bacteriap:*
17: SP archaep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	13.6	316	11	Q9D4F9
2	43	13.6	316	11	Q9D3U9
3	29	9.2	316	11	Q9EPF8
4	28	8.9	316	11	Q8VPU0
5	28	8.9	316	11	Q9EPF7
6	28	8.9	316	11	Q7TRN2
7	23	7.3	311	11	Q8VFM6
8	23	7.3	311	11	Q7TRN4
9	23	7.3	316	11	Q8VFM6
10	23	7.3	316	11	Q8VFM5
11	23	7.3	316	11	Q8VFM5
12	23	7.3	316	11	Q8VFM5
13	21	6.6	316	11	Q8VFM5
14	21	6.6	316	11	Q8VFM5
15	18	5.7	317	11	Q8VFM4
16	17	5.4	312	11	Q7TS14

17	17	5.4	315	11	Q9EPF6	Q9EPF6 mus musculus
18	17	5.4	317	11	Q7TS16	Q7TS16 mus musculus
19	17	5.4	317	11	Q7TS15	Q7TS15 mus musculus
20	15	4.7	312	11	Q8VFM6	Q8VFM6 mus musculus
21	15	4.7	313	11	Q7TS23	Q7TS23 mus musculus
22	15	4.7	313	11	Q7TRD5	Q7TRD5 mus musculus
23	15	4.7	316	11	Q8VGD1	Q8VGD1 mus musculus
24	15	4.7	327	11	Q8VFE2	Q8VFE2 mus musculus
25	14	4.4	317	4	Q8NGE0	Q8VFE2 mus musculus
26	13	4.1	172	4	Q8WZ85	Q8VFE2 mus musculus
27	13	4.1	175	11	Q55018	Q8VFE2 mus musculus
28	13	4.1	175	11	Q55019	Q8VFE2 mus musculus
29	13	4.1	175	11	Q925E9	Q8VFE2 mus musculus
30	13	4.1	215	11	Q9EP21	Q925E9 mus musculus
31	13	4.1	216	6	Q9N207	Q9EP21 mus musculus
32	13	4.1	216	6	Q9N121	Q9N207 calithrix
33	13	4.1	216	6	Q9N202	Q9N121 salmistr sci
34	13	4.1	216	6	Q9GKPF	Q9N202 calithrix
35	13	4.1	216	6	Q9N123	Q9GKPF ornithorhyn
36	13	4.1	216	6	Q9N209	Q9N123 salmistr bol
37	13	4.1	216	6	Q9GK10	Q9N209 macaca sylv
38	13	4.1	216	6	Q9GK11	Q9GK10 phasciolarc
39	13	4.1	216	6	Q9GK12	Q9GK11 ornithorhyn
40	13	4.1	216	6	Q9N213	Q9GK12 ornithorhyn
41	13	4.1	216	6	Q9N220	Q9N213 macaca sylv
42	13	4.1	216	6	Q9N205	Q9N220 eulemur ful
43	13	4.1	216	6	Q9N1Y6	Q9N205 calithrix
44	13	4.1	216	11	Q9UM32	Q9N1Y6 salmistr sci
45	13	4.1	216	11	Q9JTM18	Q9UM32 mus musculus

ALIGNMENTS

RESULT 1

Q9D4F9 PRELIMINARY; PRT; 316 AA.

AC Q9D4F9; 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE 4932441H21RLK protein.

GN 4933433E02RIK OR 4932441H21RLK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada S.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide T., Pesole G., Quackenbush J.,

RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauris P.,

RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK016560; BAB30304.1; -;

MGD; WGI:1914036; 4933433E02RIK.

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR SEQUENCE 316 AA; 34930 MW; 23189FABCB207BA CRC64;
 SQ
 Query Match 13.6%; Score 43; DB 11; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4.8e-36;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 255 ATFMVLPSSFPSPKQDNISVFYITVTPALNPLIYSLRNKEV 297
 DB 255 ATFMVLPSSFPSPKQDNISVFYITVTPALNPLIYSLRNKEV 297
 RESULT 2
 ID Q9D3U9 PRELIMINARY; PRT; 316 AA.
 AC Q9D3U9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE 4933433E02RIK protein (Olfactory receptor MOR283-1) (Olfactory
 DE receptor GA_X6K02T2PB09-9195805-9196755).
 GN 4933433E02RIK OR GA_X6K02T2PB09-9195805-9196755.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guestinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Scheenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris Y., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Young U.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Rose J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]

RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AK017036; BAB30564.1; -;
 DR EMBL: AY073025; AAB0688.1; -;
 DR EMBL: AY17822; AAF71166.1; -;
 DR MGD: MGI:1914036; 4933433E02RIK.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; F: receptor activity; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR SEQUENCE 316 AA; 34916 MW; C2C5338B675D3225 CRC64;
 SQ
 Query Match 13.6%; Score 43; DB 11; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4.8e-36;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 255 ATFMVLPSSFPSPKQDNISVFYITVTPALNPLIYSLRNKEV 297
 DB 255 ATFMVLPSSFPSPKQDNISVFYITVTPALNPLIYSLRNKEV 297
 RESULT 3
 ID Q9EPF8 PRELIMINARY; PRT; 316 AA.
 AC Q9EPF8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE T1 olfactory receptor (Olfactory receptor MOR283-11) (Olfactory
 DE receptor GA_X6K02T2PB09-9271198-9270248).
 GN GA_X6K02T2PB09-9271198-9270248.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21310002; PubMed=11416212;
 RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
 RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor
 RT loci.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Young U.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Rose J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF21234; AAG45195.1; -;
 DR EMBL: AY073740; AAL61403.1; -;
 DR EMBL: AY17827; AAF71171.1; -;

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KM RECEPTOR.
 SQ SEQUENCE 316 AA; 34981 MW; 5D89BF1BB17D480 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 29; DB 11; Length 316;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 QDNIIISVFYITVPALNPLIYSLRNKEV 297
 DB 269 QDNIIISVFYITVPALNPLIYSLRNKEV 297

RESULT 4
 Q8VGU0 PRELIMINARY; PRT; 316 AA.
 AC Q8VGU0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Olfactory receptor MOR283-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCB1_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073056; AAL60719.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KM RECEPTOR.
 SQ SEQUENCE 316 AA; 35239 MW; 2E05EB66442A34C6 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 28; DB 11; Length 316;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 QDNIIISVFYITVPALNPLIYSLRNKEV 297
 DB 270 QDNIIISVFYITVPALNPLIYSLRNKEV 297

RESULT 5
 Q9EPF7 PRELIMINARY; PRT; 316 AA.
 AC Q9EPF7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE T2 olfactory receptor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCB1_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21310002; PubMed=11416212;
 RA Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
 RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor
 loci.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
 RL EMBL; AF321234; AAG45196.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KM RECEPTOR.
 SQ SEQUENCE 316 AA; 35252 MW; B50299F5D161A1E CRC64;

Query Match
 Best Local Similarity 100.0%; Score 28; DB 11; Length 316;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 QDNIIISVFYITVPALNPLIYSLRNKEV 297
 DB 270 QDNIIISVFYITVPALNPLIYSLRNKEV 297

RESULT 6
 Q7TRN2 PRELIMINARY; PRT; 316 AA.
 AC Q7TRN2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Olfactory receptor GA_x6K02T2PB09-9255348-9255358.
 GN GA_x6K02T2PB09-9255348-9255358.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCB1_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priiddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor Esrs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY317826; AAP71170.1; -
 KM RECEPTOR.
 SQ SEQUENCE 316 AA; 35266 MW; 6318EB66443EB21D CRC64;

Query Match
 Best Local Similarity 100.0%; Score 28; DB 11; Length 316;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 QDNIIISVFYITVPALNPLIYSLRNKEV 297
 DB 270 QDNIIISVFYITVPALNPLIYSLRNKEV 297

RESULT 7
 Q8VFM6 PRELIMINARY; PRT; 311 AA.
 AC Q8VFM6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)

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DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update).
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Olfactory receptor MOR283-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073495; AAL61158.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHRDOPSN.
DR PROSITE; PSS0262; G_PROTEIN_RECPE_FL_2; 1.
KW Receptor.
SQ SEQUENCE 311 AA; 34194 MW; 90113F7C8BFD20C CRC64;

Query Match 7.3%; Score 23; DB 11; Length 311;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 SVFYITVTPALNPLIYSIRNKEV 297
DB 275 SVFYITVTPALNPLIYSIRNKEV 297

RESULT 8
Q7TRN4 PRELIMINARY; PRT; 311 AA.
AC Q7TRN4;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Olfactory receptor GA_X6K02T2PB09-9130754-9129519.
GN GA_X6K02T2PB09-9130754-9129519.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykina B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY317819; AAP71163.1; -.
DE Olfactory receptor MOR283-9 (Olfactory receptor
DE GA_X6K02T2PB09-9055944-9054994).
GN GA_X6K02T2PB09-9055944-9054994.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
SQ SEQUENCE 311 AA; 34182 MW; 1338254FA2F8D21D CRC64;

Query Match 7.3%; Score 23; DB 11; Length 311;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 SVFYITVTPALNPLIYSIRNKEV 297
DB 275 SVFYITVTPALNPLIYSIRNKEV 297

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RESULT 9
Q8VF88 PRELIMINARY; PRT; 315 AA.
AC Q8VF88;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Olfactory receptor MOR283-9 (Olfactory receptor
DE GA_X6K02T2PB09-9067220-9066273).
GN GA_X6K02T2PB09-9067220-9066273.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykina B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073646; AAL61309.1; -.
DR EMBL; AY317815; AAP71160.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHRDOPSN.
DR PROSITE; PSS0262; G_PROTEIN_RECPE_FL_2; 1.
KW Receptor.
SQ SEQUENCE 315 AA; 34927 MW; 9A9B426357BA710C CRC64;

Query Match 7.3%; Score 23; DB 11; Length 315;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GSAEDLLAFMAVDRYVAICHL 130
DB 108 GSAEDLLAFMAVDRYVAICHL 130

RESULT 10
Q8VF89 PRELIMINARY; PRT; 316 AA.
AC Q8VF89;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Olfactory receptor MOR283-8 (Olfactory receptor
DE GA_X6K02T2PB09-9055944-9054994).
GN GA_X6K02T2PB09-9055944-9054994.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
SQ SEQUENCE 316 AA; 34927 MW; 9A9B426357BA710C CRC64;

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RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Ross J.A.,
RT Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Ross J.A.,
RT Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sanders K.;

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Query Match 7.3%; Score 23; DB 11; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

108 GSAEDLLAFMAYDRYVAICHPL 130
 108 GSAEDLLAFMAYDRYVAICHPL 130

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ID 08VFMS PRELIMINARY; PRT; 316 AA.
AC 08VFMS;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Olfactory receptor MOR283-4 (Olfactory receptor
DE GA_x6K02T2PBj9-9184187-9183237).
GN GA_x6K02T2PBj9-9184187-9183237.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Ross J.A.,
RT Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sanders K.;

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RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY073497; AAL6160.1; -.
DR EMBL: AY317821; AAP71165.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN
DR PROSITE: PS50262; G_PROTEIN_RECCEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 316 AA; 35283 MW; 3D944A8FAA1A7436 CRC64;

Query Match 7.3%; Score 23; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

275 SVFYITVPALNPLIYSLRNKEV 297
275 SVFYITVPALNPLIYSLRNKEV 297

ID 09EPF5 PRELIMINARY; PRT; 319 AA.
AC 09EPF5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE T4 olfactory receptor (Olfactory receptor MOR283-7) (Olfactory
DE receptor GA_x6K02T2PBj9-9222217-92223176).
GN GA_x6K02T2PBj9-9222217-92223176.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Ross J.A.,
RT Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321234; AAG45198.1; -.
DR EMBL: AY073501; AAL6164.1; -.
DR EMBL: AY317824; AAP71168.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

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DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPS_N.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 319 AA; 35493 MW; 8CFB7EC7A5BD3D8 CRC64;
 Query Match 7.3%; Score 23; DB 11; Length 319;
 Best Local Similarity 100.0%; Pred. No. 4.1e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GSAEDLLAFMAYDRYVAICHP 130
 Db 108 GSAEDLLAFMAYDRYVAICHP 130

RESULT 13
 QTRN3 PRELIMINARY; PRT; 316 AA.
 ID QTRN3
 AC QTRN3
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Olfactory receptor GA_X6K02T2PBj9-9168355-9167405.
 GN GA_X6K02T2PBj9-9168355-9167405.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY317820; AAP71164.1; -.
 KM Receptor.
 SQ SEQUENCE 316 AA; 35091 MW; 3CFB85EC2B005D3 CRC64;
 Query Match 6.6%; Score 21; DB 11; Length 316;
 Best Local Similarity 100.0%; Pred. No. 5e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 AEDLLAFMAYDRYVAICHP 130
 Db 110 AEDLLAFMAYDRYVAICHP 130

RESULT 14
 Q8VFM4 PRELIMINARY; PRT; 317 AA.
 ID Q8VFM4
 AC Q8VFM4
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-5 (Olfactory receptor
 GN GA_X6K02T2PBj9-9119301-9118348).
 GN GA_X6K02T2PBj9-9119301-9118348.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073498; AAL61161.1; -.
 DR EMBL; AY317818; AAP71162.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPS_N.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 317 AA; 35471 MW; C5F1B706B5437F73 CRC64;
 Query Match 6.6%; Score 21; DB 11; Length 317;
 Best Local Similarity 100.0%; Pred. No. 5e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 AEDLLAFMAYDRYVAICHP 130
 Db 110 AEDLLAFMAYDRYVAICHP 130

RESULT 15
 Q8VFM3 PRELIMINARY; PRT; 315 AA.
 ID Q8VFM3
 AC Q8VFM3
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-6 (Olfactory receptor
 GN GA_X6K02T2PBj9-9092181-9091234).
 GN GA_X6K02T2PBj9-9092181-9091234.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073499; AAL61162.1; -.
 DR EMBL; AY317816; AAP71161.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS0262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 315 AA; 35179 MW; AC02001D73D1736 CRC64;

Query Match 5.7%; Score 18; DB 11; Length 315;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NSTLGGGFIIVGIINDSG 22
|||
Db 5 NSTLGGGFIIVGIINDSG 22

Search completed: October 5, 2004, 14:24:09
Job time : 120 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 14:21:12 ; Search time 41 Seconds

(without alignments)
397.898 Million cell updates/sec

Title: US-10-024-444B-2

Perfect score: 316
Sequence: 1 MELRNSTLGSGLIVGLIND.....VMAALRYLGLYLLAHLSTL 316

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	4.1	222	4 US-09-465-901-44	Sequence 44, Appl
2	13	4.1	223	4 US-09-465-901-12	Sequence 12, Appl
3	13	4.1	223	4 US-09-465-901-26	Sequence 26, Appl
4	13	4.1	223	4 US-09-465-901-46	Sequence 46, Appl
5	13	4.1	286	1 US-08-118-270-65	Sequence 65, Appl
6	13	4.1	286	5 PCT-US93-08528-65	Sequence 65, Appl
7	13	4.1	316	2 US-08-827-291A-2	Sequence 2, Appl
8	12	3.8	293	1 US-08-118-270-60	Sequence 60, Appl
9	12	3.8	293	5 PCT-US93-08528-60	Sequence 60, Appl
10	12	3.8	333	3 US-08-988-876-6	Sequence 60, Appl
11	11	3.5	222	2 US-08-467-948A-27	Sequence 27, Appl
12	11	3.5	222	3 US-08-467-948A-27	Sequence 27, Appl
13	11	3.5	224	4 US-09-465-901-30	Sequence 30, Appl
14	11	3.5	284	1 US-08-118-270-61	Sequence 61, Appl
15	11	3.5	284	5 PCT-US93-08528-61	Sequence 61, Appl
16	11	3.5	286	2 US-08-467-948A-2	Sequence 2, Appl
17	11	3.5	286	3 US-08-467-948A-2	Sequence 2, Appl
18	10	3.2	223	4 US-09-465-901-14	Sequence 14, Appl
19	10	3.2	223	4 US-09-465-901-16	Sequence 16, Appl
20	10	3.2	223	4 US-09-465-901-20	Sequence 20, Appl
21	10	3.2	223	4 US-09-465-901-24	Sequence 24, Appl
22	10	3.2	223	4 US-09-465-901-28	Sequence 28, Appl
23	10	3.2	223	4 US-09-465-901-32	Sequence 32, Appl
24	10	3.2	223	4 US-09-465-901-36	Sequence 36, Appl
25	10	3.2	223	4 US-09-465-901-40	Sequence 40, Appl
26	10	3.2	223	4 US-09-465-901-42	Sequence 42, Appl
27	10	3.2	247	1 US-08-465-980-3	Sequence 3, Appl

28	10	3.2	247	2 US-09-053-303-3	Sequence 3, Appl
29	10	3.2	247	4 US-09-339-115-3	Sequence 3, Appl
30	10	3.2	247	5 PCT-US95-07093-3	Sequence 3, Appl
31	10	3.2	269	1 US-08-118-270-64	Sequence 64, Appl
32	10	3.2	269	5 PCT-US93-08528-64	Sequence 64, Appl
33	10	3.2	274	1 PCT-US93-08528-69	Sequence 69, Appl
34	10	3.2	274	5 PCT-US93-08528-69	Sequence 69, Appl
35	10	3.2	275	1 US-08-118-270-66	Sequence 66, Appl
36	10	3.2	275	5 PCT-US93-08528-66	Sequence 66, Appl
37	10	3.2	277	1 US-08-118-270-68	Sequence 68, Appl
38	10	3.2	277	5 PCT-US93-08528-68	Sequence 68, Appl
39	10	3.2	284	1 PCT-US93-08528-67	Sequence 67, Appl
40	10	3.2	284	5 PCT-US93-08528-67	Sequence 67, Appl
41	10	3.2	314	3 US-08-988-876-7	Sequence 7, Appl
42	10	3.2	320	1 US-08-465-980-2	Sequence 2, Appl
43	10	3.2	320	2 US-09-053-303-2	Sequence 2, Appl
44	10	3.2	320	4 US-09-439-313-527	Sequence 527, App
45	10	3.2	320	4 US-09-339-115-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-465-901-44
Sequence 44, Application US/09465901
Patent No. 6492143
GENERAL INFORMATION:
APPLICANT: Reed, Randall
APPLICANT: Yau, King-Wai
TITLE OF INVENTION: Olfactory Receptor Expression Libraries
TITLE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 222
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: PCR primer
US-09-465-901-44

Query Match      4.1%; Score 13; DB 4; Length 222;
Best local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      118 MAYDRYVATCPL 130
      |||||
Db      55 MAYDRYVATCPL 67

RESULT 2
US-09-465-901-12
Sequence 12, Application US/09465901
Patent No. 6492143
GENERAL INFORMATION:
APPLICANT: Reed, Randall
APPLICANT: Yau, King-Wai
APPLICANT: Krautwurst, Dietmar
TITLE OF INVENTION: Olfactory Receptor Expression Libraries
TITLE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 57
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-12

Query Match          4.1%; Score 13; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      118 MAYDRYVAICHL 130
      |||||
Db      55 MAYDRYVAICHL 67

RESULT 3
US-09-465-901-26
; Sequence 26, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-26

Query Match          4.1%; Score 13; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      118 MAYDRYVAICHL 130
      |||||
Db      55 MAYDRYVAICHL 67

RESULT 4
US-09-465-901-46
; Sequence 46, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
```

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; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-46

Query Match          4.1%; Score 13; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      118 MAYDRYVAICHL 130
      |||||
Db      55 MAYDRYVAICHL 67

RESULT 5
US-08-118-270-65
; Sequence 65, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-65

Query Match          4.1%; Score 13; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      118 MAYDRYVAICHL 130
      |||||
Db      92 MAYDRYVAICHL 104

RESULT 6
PCT-US93-08528-65
; Sequence 65, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
```


TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-65

Query Match 4.1%; Score 13; DB 5; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHL 130
DB 92 MAYDRYVAICHL 104

RESULT 7
US-08-827-291A-2
Sequence 2, Application US/08827291A
Patent No. 5874243
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
TITLE OF INVENTION: NOVEL OLRCCL5 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GP50001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-827-291A-2

Query Match 4.1%; Score 13; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 LNPLIYSLRNKEY 297
DB 285 LNPLIYSLRNKEY 297

RESULT 8
US-08-118-270-60
Sequence 60, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-60

Query Match 3.8%; Score 12; DB 1; Length 293;

Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHP 129
Db 90 MAYDRYVAICHP 101

RESULT 9

PCT-US93-08528-60
Sequence 60, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-60

Query Match 3.8%; Score 12; DB 5; Length 293;

Best Local Similarity 100.0%; Pred. No. 0.0035;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHP 129
Db 90 MAYDRYVAICHP 101

RESULT 10

US-08-988-876-6
Sequence 6, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yee, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,876

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0441 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 333 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: Genbank

CLONE: 205814

US-08-988-876-6

Query Match 3.8%; Score 12; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MAYDRYVAICHP 129
Db 118 MAYDRYVAICHP 129

RESULT 11

US-08-467-948A-27
Sequence 27, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BUTT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-27

Query Match 3.5%; Score 11; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 YDRYVAICHPL 130
Db 60 YDRYVAICHPL 70

RESULT 12
US-08-467-947A-27
Sequence 27, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-947A-27

Query Match 3.5%; Score 11; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 YDRYVAICHPL 130
Db 60 YDRYVAICHPL 70

RESULT 13
US-09-465-901-30
Sequence 30, Application US/09465901
Patent No. 6492143
GENERAL INFORMATION:
APPLICANT: Reed, Randall
APPLICANT: Yau, King-Wai
APPLICANT: Krautwurst, Dietmar
TITLE OF INVENTION: Olfactory Receptor Expression Libraries
TITLE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 224
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: PCR primer
US-09-465-901-30

Query Match 3.5%; Score 11; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 YDRYVAICHPL 130
Db 57 YDRYVAICHPL 67

RESULT 14
US-08-118-270-61
Sequence 61, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-61

Query Match          3.5%; Score 11; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      120 YDRYVAICHPL 130
DB      95 YDRYVAICHPL 105

RESULT 15
PCT-US93-08528-61
Sequence 61, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESSES:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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MOLECULE TYPE: peptide
PCT-US93-08528-61
Query Match          3.5%; Score 11; DB 5; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      120 YDRYVAICHPL 130
DB      95 YDRYVAICHPL 105

Search completed: October 5, 2004, 14:25:40
Job time : 42 secs

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